

CC transcription factor such as c-Jun and a Stat protein such as Stat-1 and

CC Stat-3, useful for modulating gene transcription e.g., cellular

CC transformation. These identifying agents are used in the treatment of

CC dysproliferative diseases and also for treating cancer and psoriasis. A

CC Stat protein comprises the N-terminal domain, coiled-coil domain, DNA

XX binding domain, linker domain, SH2 domain and transactivation domain

SQ Sequence 271 AA;

Query Match 100.0%; Score 1388; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 2. 5e-116; Mismatches 0; Indels 0; Gaps 0;

Matches 271; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLIQLQTATAAQGGQANHPTAVTTEKQOMLEQHLDQDVREKVQDIEQKMKVVE 60

Db 1 RCLWEESRLIQLQTATAAQGGQANHPTAVTTEKQOMLEQHLDQDVREKVQDIEQKMKVVE 60

Qy 61 NLQDDDFENYKLUKSQGMQDINGNNQSVTQRMQLEQHLDQMLTAIDQMRSTIVSELAGLIS 120

Db 61 NLQDDDFENYKLUKSQGMQDINGNNQSVTQRMQLEQHLDQMLTAIDQMRSTIVSELAGLIS 120

Qy 121 AMEVYQKLTDEELADWKRPRPACTGGPPNCTIDRLENWITSLAESOLQTRQOKKLE 180

Db 121 AMEVYQKLTDEELADWKRPRPACTGGPPNCTIDRLENWITSLAESOLQTRQOKKLE 180

Qy 181 LQOKVSYKGDPVQHRPMLEERIVELFNLMSAFVVERQCPMPMHDPRPLVTKGVQFT 240

Db 181 LQOKVSYKGDPVQHRPMLEERIVELFNLMSAFVVERQCPMPMHDPRPLVTKGVQFT 240

Qy 241 TKVRLVLFPELNYQLKIKVCKIDKDSGVAA 271

Db 241 TKVRLVLFPELNYQLKIKVCKIDKDSGVAA 271

RESULT 2
AAR72082

ID AAR72082 standard; protein; 770 AA.

XX

AC AAR72082;

XX

DT 25-MAR-2003 (revised)

XX

DE 27-SEP-1995 (first entry)

XX

AC Mouse Stat3 (198f6).

XX

KM Signal transducer and activator of transcription; STAT; 198f6; Stat3;

KW receptor recognition factor; transcription factor; cellular debilitation;

KW derangement; dysfunction; interferon-gamma.

XX

OS Mus sp.

XX

PN WO9508629-A1.

XX

PD 30-MAR-1995.

XX

PP 26-SEP-1994; 94WO-US010849.

XX

PR 24-SEP-1993; 93US-00126588.

PR 24-SEP-1993; 93US-00126595.

PR 11-MAR-1994; 94US-00212184.

PR 11-MAR-1994; 94US-00212185.

PA (UYRQ) UNIV ROCKEFELLER.

XX

PI Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;

XX

DR WPI; 1995-139598/18.

XX

DR N-PSDB; A4Q89340.

PT Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.

PT XX

PS Claim 1, Page 107-110; 160pp; English.

XX A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in A4Q89338) was isolated that encoded a 91 kDa protein (A4R72080)

(Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (A4Q89339 -40) were cloned in plasmids 13af1 and 19af6 and encoded proteins termed Stat4 (A4R72081) and Stat3 (A4R72082), respectively. (Updated on 25-MAR-2003 to correct PN field.)

CC XX SQ Sequence 770 AA;

Query Match 100.0%; Score 1388; DB 2; length 770;

Best Local Similarity 100.0%; pred. No. 1e-115; Mismatches 0; Indels 0; Gaps 0;

Matches 271; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 RCLWEESRLIQLQTATAAQGGQANHPTAVTTEKQOMLEQHLDQDVREKVQDIEQKMKVVE 60

Db 1 RCLWEESRLIQLQTATAAQGGQANHPTAVTTEKQOMLEQHLDQDVREKVQDIEQKMKVVE 60

Qy 61 NLQDDDFENYKLUKSQGMQDINGNNQSVTQRMQLEQHLDQMLTAIDQMRSTIVSELAGLIS 120

Db 61 NLQDDDFENYKLUKSQGMQDINGNNQSVTQRMQLEQHLDQMLTAIDQMRSTIVSELAGLIS 120

Qy 121 AMEVYQKLTDEELADWKRPRPACTGGPPNCTIDRLENWITSLAESOLQTRQOKKLE 180

Db 121 AMEVYQKLTDEELADWKRPRPACTGGPPNCTIDRLENWITSLAESOLQTRQOKKLE 180

Qy 181 LQOKVSYKGDPVQHRPMLEERIVELFNLMSAFVVERQCPMPMHDPRPLVTKGVQFT 240

Db 181 LQOKVSYKGDPVQHRPMLEERIVELFNLMSAFVVERQCPMPMHDPRPLVTKGVQFT 240

Qy 227 AMEVYQKLTDEELADWKRPRPACTGGPPNCTIDRLENWITSLAESOLQTRQOKKLE 286

Db 227 AMEVYQKLTDEELADWKRPRPACTGGPPNCTIDRLENWITSLAESOLQTRQOKKLE 286

Qy 181 LQOKVSYKGDPVQHRPMLEERIVELFNLMSAFVVERQCPMPMHDPRPLVTKGVQFT 240

Db 181 LQOKVSYKGDPVQHRPMLEERIVELFNLMSAFVVERQCPMPMHDPRPLVTKGVQFT 240

Qy 287 LQOKVSYKGDPVQHRPMLEERIVELFNLMSAFVVERQCPMPMHDPRPLVTKGVQFT 346

Db 287 LQOKVSYKGDPVQHRPMLEERIVELFNLMSAFVVERQCPMPMHDPRPLVTKGVQFT 346

Qy 241 TKVRLVLFPELNYQLKIKVCKIDKDSGVAA 271

Db 241 TKVRLVLFPELNYQLKIKVCKIDKDSGVAA 271

RESULT 3
AAW03176

ID AAW03176 standard; protein; 770 AA.

XX

AC AAW03176;

XX

DT 24-OCT-1996 (first entry)

XX

DE Mouse STAT4.

XX

KM STAT; STAT4; signal transducer and activator of transcription;

KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;

KW autoimmune disease; antagonist; therapy.

XX

Mus sp.

XX

PP STAT; STAT4; signal transducer and activator of transcription;

KW DNA binding protein; ligand; receptor; oncogenesis; inflammation;

KW autoimmune disease; antagonist; therapy.

XX

PP WO9620954-A2.

XX

PP 11-JUL-1995.

XX

PP 28-DEC-1995; 95WO-US017025.

XX

PP 06-JAN-1995; 95US-00369796.

XX

PA (UYRQ) UNIV ROCKEFELLER.

XX

PI Darnell JE, Wen Z, Horvath CM, Zhong Z;

XX

DR WPI; 1996-333941/33.

DR	N-PSB; AAT31280.	FT	Misc-difference 713 . .714
XX		FT	/note= "Encoded by ACA CCA TTG"
PT	New STAT protein DNA-binding domain peptide(s) - useful for diagnosing, preventing or treating cellular dysfunction, e.g. oncogenesis, inflammation, parasitic disease or autoimmunity.	XX	XX
PT		PN	WO200220032-A1.
XX		PD	14-MAR-2002.
PS	Disclosure; Page 87-90; 138pp; English.	XX	PP 10-SEP-2001; 2001WO-US028254.
XX		XX	PR 08-SEP-2000; 2000US-0231212P.
CC	Mouse signal transducer and activator of transcription (STAT) protein STAT4 (AAW03176) serves a dual purpose, i.e. Signal transduction from ligand-activated receptor kinase complexes followed by nuclear translocation and DNA binding to activate transcription by nuclear STAT4 can be obt. using cDNA clone 19566 (AAT31278) obt. from splenic/thymic cells. STAT4 includes a DNA-binding domain (see also AAW0167) capable of both receptor recognition and message delivery via DNA binding in a receptor-ligand specific manner. STAT proteins and their DNA binding domains (see also AAW03165-15) are useful for screening antagonists used to inhibit STAT-mediated signal transduction and activation of transcription	PA (UY30) UNIV JOHNS HOPKINS.	PA (UY30) UNIV SOUTH FLORIDA.
CC		XX	PI Yu H, Pardoll D, Jove R, Dalton W;
CC		DR WPI; 2002-362218/39.	DR N-PSB; AAD35056.
CC		XX	PT Modulating angiogenesis and an immune response in an individual, for
XX	Sequence 770 AA;	PT	treating a hypoxic or ischaemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.
Query Match	100.0%; Score 1388; DB 2; Length 770;	XX	PT Disclosure; Page 87-89; 94pp; English.
Best Local Similarity	100.0%; Pred. No. 1e-115;	CC	The invention relates to a method of modulating angiogenesis and immune
Matches	271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	response. Method involves administering to an individual a compound that modulates the activity of signal transducer and activator of transcription
QY	1 RCLWEERSLRLOTAATAQGQGQANHPTAAVTEKQMLEQHLDQVRKVQDLEQKRVKVE 60	CC	3 (STAT3). Modulating angiogenesis is useful for treating or preventing
Db	107 RCLWEERSLRLOTAATAQGQGQANHPTAAVTEKQMLEQHLDQVRKVQDLEQKRVKVE 166	CC	hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, hypoglycaemia, nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Suppressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating
AAE2055		CC	specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrosarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human
ID	AAE22055 standard; protein; 720 AA.	CC	statobeta protein
XX		XX	Sequence 720 AA;
AC	AAE22055;	Query Match	99.2%; Score 1377; DB 5; Length 720;
XX	25-JUL-2002 (first entry)	Best Local Similarity	99.3%; Pred. No. 9.1e-15;
DT		Matches	1; Mismatches 1; Indels 0; Gaps 0;
XX	Human Stat3beta protein.	QY	1 RCLWEERSLRLOTAATAQGQGQANHPTAAVTEKQMLEQHLDQVRKVQDLEQKRVKVE 60
DE		Db	107 RCLWEERSLRLOTAATAQGQGQANHPTAAVTEKQMLEQHLDQVRKVQDLEQKRVKVE 166
XX		QY	61 NLQDDDPNYKLKSQGMDQDLNGNQSUTRKMQQLEQHLDQMRSSVSELAGLIS 120
Human: signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; inflammation; chronic obstructive pulmonary disease; embolism; respiratory distress syndrome; hypoxia; stroke; angiogenesis; myocardial infarction; hypoglycaemia; insulin dependent diabetes mellitus; emphysema; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitroglycerin; necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polyarthrosis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; gene; lesion; Statbeta.	Db	167 NLQDDDPNYKLKSQGMDQDLNGNQSUTRKMQQLEQHLDQMRSSVSELAGLIS 226	
OS	Homo sapiens.	QY	121 AMEVYQKLTBELADWKRRQIACTGGPPNCLDRLENWITSLASQLTRQIKLEE 180
XX		Db	227 AMEVYQKLTBELADWKRRQIACTGGPPNCLDRLENWITSLASQLTRQIKLEE 286
FH			
Key	Location/Qualifiers		

Db	287	LQOKVSTKGDPVQHRLMLERIVELFRNLMSAFWVERQCPMPMHDPRPLVIKGVQFT 346	Qy	121	AMYVQKLTDELAQDKRPIATCGPPNCLDRLENWTSLAESLOQTQQIKLLE 180
Db	241	TKVLILYKEPEALNYQLKIKVCTIDKDSGVAA 271	Qy	241	TKVLILYKEPEALNYQLKIKVCTIDKDSGVAA 271
Db	347	TKVLILYKEPEALNYQLKIKVCTIDKDSGVAA 377	Qy	181	LQOKVSTKGDPVQHRLMLERIVELFRNLMSAFWVERQCPMPMHDPRPLVIKGVQFT 240
Db	287	LQOKVSTKGDPVQHRLMLERIVELFRNLMSAFWVERQCPMPMHDPRPLVIKGVQFT 346	Qy	241	TKVLILYKEPEALNYQLKIKVCTIDKDSGVAA 271
Db	347	TKVLILYKEPEALNYQLKIKVCTIDKDSGVAA 377	Qy	121	AMYVQKLTDELAQDKRPIATCGPPNCLDRLENWTSLAESLOQTQQIKLLE 180
RESULT 5					
DBB57164	ID	ABB57164 standard; protein; 769 AA.	AC	ABB57164;	XX
XX	DT	07-MAR-2002 (first entry)	DE	XX	XX
Mouse ischaemic condition related protein sequence SEQ ID NO:398.	DE	XX	DE	XX	XX
Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.	KW	XX	KW	XX	XX
Mus musculus.	OS	XX	OS	XX	XX
WO200188188-A2.	PN	XX	PN	XX	XX
22-NOV-2001.	PD	XX	PD	XX	XX
18-MAY-2001; 2001WO-JP004192.	PA	XX	PA	XX	XX
18-MAY-2000; 2000JP-00145977.	PR	XX	PR	XX	XX
(UNIV) UNIV NIHON SCHOOL JURIDICAL PERSON.	PA	XX	PA	XX	XX
Ishikawa K., Abai S., Takahashi Y., Nagata T., Ishii Y.; WPI; 2002-034733/04.	PT	XX	PT	XX	XX
N-PSDB; ABI99454.	DR	XX	DR	XX	XX
Claim 2; Page 1084-1087; 2690pp; English.	PS	XX	PS	XX	XX
The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI9912, encoding the expression sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention	CC	CC	CC	CC	CC
Sequence 769 AA;	SQ	XX	XX	XX	XX
Query Match 99.2%; Score 1377; DB 5; length 769; Best Local Similarity 99.3%; Pred. No. 1e-114; Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	XX	XX	XX	XX	XX
1 RCLWEBSRLLQTAATAQG3QANHPTAAVTEKQMLQHODVRVQDLEQKRVVE 60	CC	CC	CC	CC	CC
107 RCLWEBSRLLQTAATAQG3QANHPTAAVTEKQMLQHODVRVQDLEQKRVVE 166	CC	CC	CC	CC	CC
61 NLQDDDFNYKILKSDQMDINGNNQSVTQKMQLEQMLTALDMRRSVELAGLIS 120	CC	CC	CC	CC	CC
RESULT 6					
AEE22054	ID	AAE22054 standard; protein; 769 AA.	AC	AAE22054;	XX
25-JUL-2002 (first entry)	DT	XX	DT	XX	XX
Human Stat3 protein.	DE	XX	DE	XX	XX
Human; signal transducer and activator of transcription 3; ischaemia; immune response; Stat3; coronary atherosclerosis; vascular occlusion; hypoxia; stroke; angiogenesis; myocardial infarction; Hypoglycaemia; inflammation; chronic obstructive pulmonary disease; cardiac arrest; insulin dependent diabetes mellitus; hypoxia; trauma; scleroderma; shock; chronic active hepatitis; adult respiratory distress syndrome; nitrogen necrosis; proliferative angiopathy; autoimmune thyroiditis; Sjogren's syndrome; multiple sclerosis; Addison's disease; epilepsy; polyposis; rheumatoid arthritis; autoimmune infertility; anaemia; proliferative disease; Grave's disease; ulcerative colitis; sarcoma; carcinoma; degenerative disorder; gene therapy; growth deficiency; cirrhosis; hypoproliferative disorder; lesion.	KW	XX	KW	XX	XX
Homo sapiens.	OS	XX	OS	XX	XX
WO200220032-A1.	PN	XX	PN	XX	XX
14-MAR-2002.	PD	XX	PD	XX	XX
10-SEP-2001; 2001WO-US028254.	PF	XX	PF	XX	XX
08-SEP-2000; 2000US-0231212P.	PR	XX	PR	XX	XX
(UWJO) UNIV JOHNS HOPKINS.	PA	XX	PA	XX	XX
Yu H., Pardoll D., Jove R., Dalton W.; WPI; 2002-362218/39.	PT	XX	PT	XX	XX
N-PSDB; AAD35065.	DR	XX	DR	XX	XX
Modulating angiogenesis and an immune response in an individual, for treating a hypoxic or ischaemic condition, comprises administering a compound that modulates the activity of a signal transducer and activator of transcription 3.	PT	XX	PT	XX	XX
Disclosure; Page 83-85; 94pp; English.	PS	XX	PS	XX	XX
The invention relates to a method of modulating angiogenesis and immune response. Method involves administering to an individual a compound that modulate the activity of signal transducer and activator of transcription 3 (Stat3). Modulating angiogenesis is useful for treating or preventing hypoxic or ischaemic condition or disorder which is the result of stroke, ischaemia, coronary atherosclerosis, myocardial infarction, inflammation, tissue ischaemia in the lower extremities, infarction, trauma, vascular occlusion, prenatal or postnatal oxygen deprivation, suffocation, shock, chronic obstructive pulmonary disease, choking, asphyxia, hypoglycaemia, epilepsy, emphysema, adult respiratory distress syndrome, cardiac arrest,	CC	CC	CC	CC	CC

CC nitrogen necrosis, proliferative angiopathy e.g. diabetic microangiopathy with neovascularisation. Supressing an immune response is useful for ameliorating a symptom of an autoimmune disease such as systemic lupus erythematosus, multiple sclerosis, insulin dependent diabetes mellitus, Sjogren's syndrome, scleroderma, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive enteropathy, autoimmune neutropenia, myasthenia gravis, idiopathic thrombocytopenia purpura, Grave's disease, Goodpasture's disease, rheumatoid arthritis, cirrhosis, pemphigus vulgaris, autoimmune infertility, bullous pemphigoid, discoid lupus, ulcerative colitis and dense deposit disease. The method is useful in preventing or treating specific proliferative and oncogenic disease which includes sarcomas and carcinomas e.g., bladder carcinoma, colon carcinoma, chronic leukaemia, fibrocarcoma, liposarcoma, degenerative disorders, growth deficiency, hypoproliferative disorders, physical trauma, lesions and wounds. The method is also used in gene therapy. The present sequence is human Stat3 protein

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.2%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271
Db	347	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	377

RESULT 7

XX AAE22056 standard; protein; 769 AA.

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.2%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	180
Db	227	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	286
QY	181	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	240
Db	287	LOOKVSYKGDPIVQHMPMLEERIVELFRNLMSAFVVERQCPMPMPDRPLVTKVQFT	346
QY	241	TKRVLVVKPPELYNQLKIKVCIKDSDGVAA	271

XX SQ Sequence 769 AA:

Query Match	Score	DB	Length
Best Local Similarity	99.3%	5	769;
Matches	269;	Pred. No.	1e-114;
		Indels	1;
		Gaps	0;
QY	1	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	60
Db	107	RCLWEESSLQIQTAAQGGQANHPTAAVTEKQMLEQHQDVKRVDQLEOKKVVE	166
QY	61	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	120
Db	167	NLQDDDFENYKILKSQGMDQDINGNNQSVTQKMQLEQMLTALDQMRSTVSELAGLLS	226
QY	121	AMEYVQKLTDBELAKRKRQBIACTCGPPNCLDRLENWTSLASQLOTRQQKKLEE	1

Db	347 TKVRLLVKFPPELNQQLKIKVCLDKDSDVAA 377	Db	347 TKVRLLVKFPPELNQQLKIKVCLDKDSDVAA 377
RESULT 8		RESULT 9	
AAR82395	AAR82395 standard; protein; 770 AA.	ID	AAY03768
XX		ID	AAY03768 standard; protein; 770 AA.
AC	AAR82395;	XX	
XX		AC	AAY03768;
DT	25-MAR-1995 (first entry)	XX	
XX	DR Mouse liver acute phase response factor.	DT	11-JUN-1999 (first entry)
XX		XX	
KW	Mouse; acute phase response factor; transcription factor; interleukin-6;	DE	Human STAT3 allelic variant.
KW	signal transmission; liver; antibody; antisense; ribozyme;	XX	
KW	antiinflammatory; antitumor; hypotensive; therapy.	KW	Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6; intracellular transcription factor; interleukin-6; medicament; variant; pharmaceutical; autoimmune disease; inflammatory; human.
OS	Mus musculus.	XX	
XX		OS	Homo sapiens.
PN	EP676469-A2.	XX	
XX		PN	EP905234-A2.
PD	11-OCT-1995.	XX	
XX		PD	31-MAR-1999.
PF	29-MAR-1995; 95EP-00104670.	XX	
XX		PF	18-FEB-1998; 98EP-00102774.
PR	04-APR-1994; 94JP-00065825.	XX	
XX		PR	16-SEP-1997; 97EP-00116061.
PA	(KISHI/) KISHIMOTO T.	XX	
XX		PA	(ISTP) ARS APPLIED RES SYSTEMS HOLDING NV.
PT	Akira S, Kishimoto T;	XX	
XX		PT	Serlupi-Crescenzi O, Della Pietra L;
DR	WPI; 1995-346089/45.	XX	
DR	N-PSDB; AAT05619.	DR	WPI; 1999-192664/17.
XX		DR	N-PSDB; AAX29281.
PT	New acute phase response factor - for developing inhibitory agents for treating diseases induced by cytokine(s) such as IL-6, e.g. inflammatory diseases.	XX	
PT		PT	New human Signal Transducer and Activator of Transcription 3 (STAT3) allelic variant useful for treatment of autoimmune and inflammatory disease.
XX		PT	
PS	claim 10; Page 20-22; 31PP; English.	PS	Claim 2; Page 9-13; 32PP; English.
XX		XX	
CC	The sequence represents a mouse acute phase response factor (APRF), a transcription factor related to signal transmission of interleukin-6 (IL-6). The protein is encoded by a cDNA, isolated from a mouse liver cDNA library using a polymerase chain reaction product (amplified using primers derived from an IL-6-treated mouse liver peptide) as a probe.	CC	The present sequence represents a predominant allelic variant of human Signal Transducer and Activator of Transcription 3 (STAT3) protein, an intracellular transcription factor which mediates IL-6 signals. The encoding sequence differs from the original published human STAT3 gene sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3 DNA molecule can be used for the recombinant expression of the variant. STAT3 protein is useful as a medicament or pharmaceutical composition for treatment of autoimmune or inflammatory disease. ^B
CC		CC	
CC	ribozymes, may be used to treat diseases induced by IL-6, e.g. inflammatory disease, leukemia, cancer, osteoclasia, pulmonary hypertension, etc	CC	
CC		CC	
XX	Sequence 770 AA;	XX	Sequence 770 AA;
SQ		SQ	
Query Match	Best Local Similarity 99.2%; Score 1377; DB 2; Length 770; Matches 269; Conservative 1; Mismatches 0; Gaps 0;	Query Match	Best Local Similarity 99.2%; Score 1377; DB 2; Length 770; Matches 269; Conservative 99.3%; 1; Mismatches 1; Indels 0; Gaps 0;
OY	1 RCLWEESSLRQLQATAAQGQGANHPTAVTEKQMLEQHQDVVRKVQDLEKQMVKE 60	OY	1 RCLWEESSLRQLQATAAQGQGANHPTAVTEKQMLEQHQDVVRKVQDLEKQMVKE 60
Db	107 RCLWEESSLRQLQATAAQGQGANHPTAVTEKQMLEQHQDVVRKVQDLEKQMVKE 166	Db	107 RCLWEESSLRQLQATAAQGQGANHPTAVTEKQMLEQHQDVVRKVQDLEKQMVKE 166
OY	61 NLQDDDFENYKTKLKSQGMDQDINGANNOVSTRQKQMLEQHQLTALDQRRTSVSELAGILS 120	OY	61 NLQDDDFENYKTKLKSQGMDQDINGANNOVSTRQKQMLEQHQLTALDQRRTSVSELAGILS 120
Db	167 NLQDDDFENYKTKLKSQGMDQDINGANNOVSTRQKQMLEQHQLTALDQRRTSVSELAGILS 226	Db	167 NLQDDDFENYKTKLKSQGMDQDINGANNOVSTRQKQMLEQHQLTALDQRRTSVSELAGILS 226
OY	121 AMEVYQKLTDEBLADNRRTPETACIGGPNTICLDRLENWITSLAESQLQTROQIKLLE 180	OY	121 AMEVYQKLTDEBLADNRRTPETACIGGPNTICLDRLENWITSLAESQLQTROQIKLLE 180
Db	227 AMEVYQKLTDEBLADNRRTPETACIGGPNTICLDRLENWITSLAESQLQTROQIKLLE 286	Db	227 AMEVYQKLTDEBLADNRRTPETACIGGPNTICLDRLENWITSLAESQLQTROQIKLLE 286
OY	181 LQOKVSKGDPVQHREPMLEERIVELFRNLMSAFVVERQPMPMHPDRPLVTKTGQFT 240	OY	181 LQOKVSKGDPVQHREPMLEERIVELFRNLMSAFVVERQPMPMHPDRPLVTKTGQFT 240
Db	287 LQOKVSKGDPVQHREPMLEERIVELFRNLMSAFVVERQPMPMHPDRPLVTKTGQFT 346	Db	287 LQOKVSKGDPVQHREPMLEERIVELFRNLMSAFVVERQPMPMHPDRPLVTKTGQFT 346
OY	241 TKVRLLVKFPPELNQQLKIKVCLDKDSDVAA 271	OY	241 TKVRLLVKFPPELNQQLKIKVCLDKDSDVAA 271

CC the control of a promoter containing at least two adjacent weak binding sites for STAT protein dimers. The methods are used for identifying new drugs. An antagonist of STAT N-terminal dimeric interactions that inhibits the binding of the STAT dimers to adjacent weak binding sites on a promoter of a gene, could be useful as drugs in the treatment of diseases, e.g. inflammation, allergy, asthma and leukaemia. On the other hand, an agonist of N-terminal dimeric interactions between STAT dimers, can be used as drugs in the treatment of diseases e.g. anaemia, neutropaenia, thrombocytopaenia, cancer, obesity, viral diseases and growth retardation. The present sequence is murine STAT3 protein

XX Sequence 770 AA;

SQ Query Match 99.2%; Score 1377; DB 5; Length 770; Best Local Similarity 99.3%; Pred. No. 1e-114; Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

QY 1 RCLMEBESRLQLQTATAAQOGGQANHPTAVVTEKQOMLEQHLDQVRKVQDLEQRMKVE 60
Db 107 RCLWEESRLQLQTATAAQOGGQANHPTAVVTEKQOMLEQHLDQVRKVQDLEQRMKVE 166

QY 61 NLQDDPFENYKTLKSQGMDLNGNNSYTRQKQMLTAQDRSIVSELAGLLS 120
Db 167 NLQDDPFENYKTLKSQGMDLNGNNSYTRQKQMLTAQDRSIVSELAGLLS 226

QY 121 AMEVYQKLTDEBLADWKRQIAICGGPPNCLDRLENWITSLAQLQTQIKULE 180
Db 227 AMEVYQKLTDEBLADWKRQIAICGGPPNCLDRLENWITSLAQLQTQIKULE 286

QY 181 LQOKVSKYKGDPVQHRPMLBERVELFNLMSAFVVERQPOMPMHDPLPVTKIGQFT 240
Db 287 LQOKVSKYKGDPVQHRPMLBERVELFNLMSAFVVERQPOMPMHDPLPVTKIGQFT 346

Db 347 TKVRLLVKFPPELNVYQLKIKVCIDKSDGVAA 377

RESULT 12

ID ABG69497 standard; protein; 770 AA.

AC ABG69497;
XX DT 21-OCT-2002 (first entry)
XX DE Human bait protein SPAT3.
XX KW Human; Yeast two-hybrid assay; adipocyte; bait protein; NIDDM; non-insulin diabetes mellitus; obesity; selected interacting domain; SID; protein-protein interaction map; PIM; anorectic; metabolic disorder.
XX OS Homo sapiens.
XX PN WO200253726-A2.

XX PD 11-JUL-2002.
XX PP 28-DEC-2001; 2001WO-EP015423.

XX PR 02-JAN-2001; 2001US-0259377P.

XX PA (HYBR-) HYPERGENICS.
PA (CNRS) CENT NAT RECH SCI.

XX PI Leigrain P, Marullo S, Jockers R;
XX DR WPI; 2002-583612/62.
XX N-PSDB; ABS51033.

XX PT Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders.

XX Claim 1; Page 54; 125pp; English.

XX The invention relates to a complex of protein-protein interactions that

CC defined in the specification, or polynucleotides in adipocytes encoding for the polypeptides. Also included are a recombinant cell expressing the interacting polypeptides and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective medium containing a modulating compound and a reporter gene the expression of which is toxic for the recombinant host cell which is

CC transformed with two vectors, where the first vector comprises a polynucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polynucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the growth of the recombinant host cell (i.e. using the yeast two-hybrid system). The

CC complexes are useful for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The compound isolated by the method is useful for treating and preventing obesity or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID. The present sequence represents a member of the protein complex of the invention, used as the bait protein in the yeast two-hybrid assay

XX Sequence 770 AA;

SQ Query Match 99.2%; Score 1377; DB 5; Length 770; Best Local Similarity 99.3%; Pred. No. 1e-114; Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0; CC

QY 1 RCLWEESRLQLQTATAAQOGGQANHPTAVVTEKQOMLEQHLDQVRKVQDLEQRMKVE 60
Db 107 RCLWEESRLQLQTATAAQOGGQANHPTAVVTEKQOMLEQHLDQVRKVQDLEQRMKVE 166

QY 61 NLQDDPFENYKTLKSQGMDLNGNNSYTRQKQMLTAQDRSIVSELAGLLS 120
Db 167 NLQDDPFENYKTLKSQGMDLNGNNSYTRQKQMLTAQDRSIVSELAGLLS 226

QY 121 AMEVYQKLTDEBLADWKRQIAICGGPPNCLDRLENWITSLAQLQTQIKULE 180
Db 227 AMEVYQKLTDEBLADWKRQIAICGGPPNCLDRLENWITSLAQLQTQIKULE 286

QY 181 LQOKVSKYKGDPVQHRPMLBERVELFNLMSAFVVERQPOMPMHDPLPVTKIGQFT 240
Db 287 LQOKVSKYKGDPVQHRPMLBERVELFNLMSAFVVERQPOMPMHDPLPVTKIGQFT 346

Db 347 TKVRLLVKFPPELNVYQLKIKVCIDKSDGVAA 377

RESULT 13

ID ABU10476 standard; protein; 770 AA.

AC ABU10476;
XX DT 06-AUG-2003 (first entry)
XX DE Mouse STAT3 protein.

XX KW Mouse; signal transducer and activator of transcription; drug design; drug screening; STAT-STAT dimer interaction; STAT3.

XX OS Mus sp.

XX FI Key Location/Qualifiers 4..9
FI Region /label= alpha_helix_1
FT Region 12..21

FT /label= alpha_helix_2
 FT /note= "Residues 19-21 form a 3 helix"
 FT Region
 FT /label= alpha_helix_3
 FT 35. .40
 FT /label= alpha_helix_4
 FT 43. .47
 FT /label= alpha_helix_5
 FT 50. .73
 FT /label= alpha_helix_6
 FT /note= "Residues 57, 61, 64, 68 and 71 contribute to packing of the coiled-coil"
 FT 77. .96
 FT /label= alpha_helix_7
 FT /note= "Residues 79, 83, 86, 90 and 94 contribute to packing of the coiled-coil"
 FT 99. .119
 FT /label= alpha_helix_8

XX US2003003563-A1.
 XX PN 02-JAN-2003.
 XX PD 19-OCT-2001; 2001US-00045792.
 XX PR 23-JAN-1998; 98US-00012710.
 XX PR 24-APR-2000; 2000US-00556273.
 PA (VINK/) VINKEMEIER U.
 PA (MOAR/) MOAREFI I.
 PA (DARN/) DARNELL J E.
 PA (KURI/) KURIYAN J.

XX WPI; 2003-447354/42.

XX New crystal having an N-terminal domain of a STAT protein performing X-ray crystallographic studies, useful for screening drugs that enhance or inhibit STAT-STAT dimer interactions.

XX disclosure; page 25-26; 46pp; English.

XX The invention relates to a crystal of an N-terminal domain of signal transducer and activator of transcription (STAT) protein, where the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the N-terminal domain of the STAT protein to a resolution of greater than 5.0 angstrom. The methods and compositions are useful for the design and screening of drugs that enhance or inhibit STAT-STAT dimer interactions. The present sequence represents the amino acid sequence of mouse STAT3 protein.

XX Sequence 770 AA;

Query Match Score 99.2%; Score 1377; DB 6; Length 770;
 Best Local Similarity 99.3%; Pred. No. 1e-114; 1; Indels 0; Gaps 0; Matches 269; Conservative 1; Mismatches 1;

QY 1 RCLWEESELQIQTATAAQCGQANHPTAAVTEKQOMLEQHQDQYRKWQDLEQKMKW 60
 Db 107 RCLWEESELQIQTATAAQCGQANHPTAAVTEKQOMLEQHQDQYRKWQDLEQKMKW 166

QY 61 NLQDDDFDNKYKTLKSQGDMDQDINGNNSVTROKQQLQEMTALDQMRSTIVSELAGLS 120
 Db 167 NLQDDDFDNKYKTLKSQGDMDQDINGNNSVTROKQQLQEMTALDQMRSTIVSELAGLS 226

QY 121 AMEVYQKULTDEELADWKRQPKLACIGGPPNTCLDRLENWITSLAESOLQTROQKLEE 180
 Db 227 AMEVYQKULTDEELADWKRQPKLACIGGPPNTCLDRLENWITSLAESOLQTROQKLEE 286

QY 181 LQQKYSKDPPIVHRPMFERIVELFRNLMSAFVVERQPQCPMPHPDRPLVIKGVOFT 240
 Db 287 LQQKYSKDPPIVHRPMFERIVELFRNLMSAFVVERQPQCPMPHPDRPLVIKGVOFT 346

QY 241 TKVRLUVKPELNQKIKVCIIDSGDVA 271
 Db 347 TKVRLUVKPELNQKIKVCIIDSGDVA 377

RESULT 14
 ADN04365
 ID ADN04365 standard; protein; 770 AA.
 XX
 AC ADN04365;
 XX DT 01-JUL-2004 (first entry)
 DE Antipsoriatic protein sequence #377.
 XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.
 XX OS Homo sapiens.
 XX PN WO2004028479-A2.
 XX PD 08-APR-2004.
 XX PF 25-SEP-2003; 2003WO-US031907.
 XX PR 25-SEP-2002; 2002US-0414006P.
 PA (GETH) GENENTECH INC.
 XX PT Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;
 DR N-PSDB; ADN04364.
 XX WPI; 2004-305105/28.
 PT New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a PT mammal.
 XX PS Claim 9; SEQ ID NO 759; 3069pp; English.
 XX The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
 XX SQ Sequence 770 AA;
 Query Match Score 99.2%; Score 1377; DB 8; Length 770;
 Best Local Similarity 99.3%; Pred. No. 1e-114; 1; Indels 0; Gaps 0; Matches 269; Conservative 1; Mismatches 1;

QY 1 RCLWEESELQIQTATAAQCGQANHPTAAVTEKQOMLEQHQDQYRKWQDLEQKMKW 60
 Db 107 RCLWEESELQIQTATAAQCGQANHPTAAVTEKQOMLEQHQDQYRKWQDLEQKMKW 166

QY 61 NLQDDDFDNKYKTLKSQGDMDQDINGNNSVTROKQQLQEMTALDQMRSTIVSELAGLS 120
 Db 167 NLQDDDFDNKYKTLKSQGDMDQDINGNNSVTROKQQLQEMTALDQMRSTIVSELAGLS 226

QY 121 AMEVYQKULTDEELADWKRQPKLACIGGPPNTCLDRLENWITSLAESOLQTROQKLEE 180
 Db 227 AMEVYQKULTDEELADWKRQPKLACIGGPPNTCLDRLENWITSLAESOLQTROQKLEE 286

QY 181 LQQKYSKDPPIVHRPMFERIVELFRNLMSAFVVERQPQCPMPHPDRPLVIKGVOFT 240
 Db 287 LQQKYSKDPPIVHRPMFERIVELFRNLMSAFVVERQPQCPMPHPDRPLVIKGVOFT 346

QY 241 TKVRLUVKPELNQKIKVCIIDSGDVA 271
 Db 347 TKVRLUVKPELNQKIKVCIIDSGDVA 377

RESULT 15
 ID AAB58442 standard; protein; 793 AA.
 XX
 AC AAB58442;
 XX
 DT 14-MAR-2001 (first entry)
 XX Lung cancer associated polypeptide sequence SEQ ID 780.
 XX Human; lung cancer associated protein; neuroprotective; cytostatic;
 KW cardioactive; immunomodulatory; muscular active; pulmonary;
 KW gastrointestinal; nephroprotective; antinefrective; gynecological;
 KW antibacterial; diagnostic; neural disorder; immune disorder; reproductive;
 KW proliferative disorder; wound healing; infectious disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2000055180-A2.
 XX
 PD 21-SEP-2000.
 XX
 PP 08-MAR-2000; 2000WO-US005918.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 DR N-PSDB; AAF18318.
 XX
 PT Lung cancer associated gene sequences, referred to as lung cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as lung cancer.
 XX
 PS Claim 11; Page 1310-1313; 1425pp; English.
 XX
 CC Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
 CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
 CC associated proteins and polynucleotide sequences, their agonists, and
 CC antagonists may have neuroprotective; cytoprotective; cardioactive;
 CC immunomodulatory; muscular active; general; vulnerary; gastrointestinal
 CC general; nephroprotective; anti-infective; gynecological; or antibacterial
 CC activity. The invention also includes antibodies specific for the protein
 CC or polynucleotide sequences. The lung cancer associated polynucleotide
 CC sequences may be used for detection of lung cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The proteins may be used to treat disorders such as
 CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
 CC cardiovascular, renal, and proliferative disorders. The proteins may also
 CC be used in the treatment of wounds and infectious diseases.
 CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
 CC used in the course of the invention for the identification and
 CC characterisation of the polynucleotide and protein sequences
 XX
 SQ Sequence 793 AA;

Query Match 99.2%; Score 1377; DB 3; length 793;
 Best Local Similarity 99.3%; Pred. No. 1e-114; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 269; Conservative 1;

QY	1	RCLWEESRLQLQATAAQGGQANHPTAAWTRKQOMLHQHIVDVRKRVQDIBQMKVWE	60
Db	130	RCLWEESRLQLQATAAQGGQANHPTAAWTRKQOMLHQHIVDVRKRVQDIBQMKVWE	189
QY	61	NIQQDDDFPNYKTLKQSQDMQDINGNNNSVTROKMQLEQMLTALDQMRRTSVSLAGILS	120
Db	190	NIQQDDDFPNYKTLKQSQDMQDINGNNNSVTROKMQLEQMLTALDQMRRTSVSLAGILS	249

Db 167 NLQDPDFPNYKILKSQMDLNGNNQSVTQKMQLEQMLTAIDMRRSIVSELAGLIS 226
QY 121 AMYVQKLTIDBLADWRRPPIACTIGGPPNIFCLDRLENWITSLASQLOTRQQIKLLE 180
Db 227 AMYVQKLTIDBLADWRRPPIACTIGGPPNIFCLDRLENWITSLASQLOTRQQIKLLE 286
QY 181 IQQKVSYKGDPVQHPRMLEERVELFRNTMSAFVTERQPCMPMPDRPLVIKTVQFT 240
Db 287 IQQKVSYKGDPVQHPRMLEERVELFRNLMSAFVVERQPCMPMPDRPLVIKTVQFT 346
QY 241 TWRLLVKEPEINYQLKIKVCDKSDGVAA 271
Db 347 TWRLLVKEPEINYQLKIKVCDKSDGVAA 377

RESULT 2

STA3_HUMAN STANDARD; PRT; 770 AA.

ID STA3_HUMAN STANDARD; PRT; 770 AA.

AC P40763; O49116; Q9BW4;

DT 01-FEB-1995 (Rel. 31, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Signal transducer and activator of transcription 3 (Acute-phase response factor).

GN STAT3; Synonyms=APRF;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9605;

RL [1]

RN SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Placenta;

RX MEDLINE=94208062; PubMed=7512451;

RA Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T., RA Yoshida K., Sudo T., Narita M., Kishimoto T.;

RT "Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling pathway."; RL Cell 77:63-71(1994).

RN [12]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX MEDLINE=93296260; PubMed=9630560;

RA Della Pietra L., Bressan A., Pezzotti A., Serlupi-Crescenzi O.;

RT "Highly conserved amino-acid sequence between murine STAT3 and a revised human STAT3 sequence."; RL Gene 213:119-124(1998).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM DBL-701), AND VARIANT ILE-143.

RA Rieder M.J., Daniels R.L., da Fonte S.H., Hastings N.C., Ahearn M.O., RA Rajkumar N., Yi Q., Nickerson D.A.;

RT "SeattleSPS: NHLBI HU66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu)."; RT Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

RL [4]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND DBL-701).

RC TISSUE=Kidney, and Pancreas;

RX MEDLINE=22388057; PubMed=12477932; DOI=10.1073/pnas.242603999;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schulz G.D., RA Altschul S.F., Zeeberg B., Butow K.H., Scheaffer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsien F., RA Hopkinson D.K., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Ronald M.P., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J., RA Bosak S.A., Mcowan P.J., McKernan K.J., Malek A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay J.J., Rulyk S.W., RA Villalon D.K., Muzny D.M., Soerergren E.J., Lu X., Gibbs R.A., RA Fahey J., Heitman B., Keetman M., Madan A., Rodriguez S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grinshaw J., Schmutz J., Myers R.M., RA Butterfield Y.S.N., Kirzynski M.I., Skalska U., Smailus D.E., RA

RX Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RX "Generation and initial analysis of more than 15,000 full-length human
RX and mouse cDNA sequences";
RX Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RX [15]

RX SEQUENCE OF 564-704 FROM N.A.

RX Della Pietra L., Bressan A., Pezzotti A.R., Serlupi-Crescenzi O.;

RX Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RX [6]

RX PHOSPHORYLATION ON SERINE.

RX MEDLINE=95215843; PubMed=7701321;

RX Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;
RX "Requirement of serine phosphorylation for formation of STAT-promoter complexes";
RX Science 267:1950-1954 (1995).

CC CC acute-phase responsive elements identified in the promoters of various acute-phase protein genes.

CC CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.

CC CC -!- SUBUNIT: forms a homodimer or a heterodimer with a related family member (at least STAT1).

CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.

CC CC -!- ALTERNATIVE PRODUCTS:

CC CC Event=Alternative splicing; Named isoforms=2;

CC CC Name=1;

CC CC IsoID=P40763-1; Sequence=Displayed;

CC CC Name=Del-701;

CC CC IsoID=P40763-2; Sequence=VSP 010474;

CC CC -!- TISSUE SPECIFICITY: Heart, brain, placenta, lung, liver, skeletal muscle, kidney and pancreas.

CC CC -!- PTM: Tyrosine phosphorylation in response to IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity.

CC CC -!- SIMILARITY: Belongs to the transcription factor STAT family.

CC CC -!- SIMILARITY: Contains 1 SH2 domain.

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DR EMBL; I29277; AA8374.1; .-.

DR EMBL; AJ012463; CAI10032.1; .-.

DR EMBL; AY572796; AA66986.1; .-.

DR EMBL; BC00627; AAH00627.1; .-.

DR EMBL; BC014482; AAH14482.1; .-.

DR EMBL; AF029311; AAH84254.1; .-.

DR EMBL; A54444; AA54444.

DR HSSP; P42227; IBGI.

DR TRANSFAC; To1493; .-.

DR MIM; 102502; .-.

DR Genew; HGNC:11364; STAT3.

DR GO; GO:0005737; C:cytoplasm; TAS.

DR GO; GO:0005341; C:nucleus; TAS.

DR GO; GO:0005062; F:hematopoietin/interviferon-class (D200-domain. . . ; TAS.

DR GO; GO:0003700; F:transcription factor activity; TAS.

DR GO; GO:0006928; P:cell motility; TAS.

DR GO; GO:0007259; P:JAK-STAT cascade; TAS.

DR GO; GO:000122; P:negative regulation of transcription from P. . . ; TAS.

DR GO; GO:0007399; P:neurogenesis; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR008967; P53_like_DNA_bnd.

DR InterPro; IPR001217; STAT.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF02864; STAT_bind; 1.

DR Pfam; PF02864; STAT_alpha; 1.

DR	Pfam: PF02865; STAT int; 1.	RC	TISSUE=Thymus;	
DR	PROSINE; PS5001; SH2; 1.	RX	MEDLINE=9418878; PubMed=8140422;	
KW	Activator; Alternative splicing; DNA-binding; Nuclear protein;	RA	Zhong Z., Wen Z., Darnell J.E. Jr.;	
KW	Phosphorylation; Polymorphism; SH2 domain; Transcription regulation.	RT	"Stat3: a STAT family member activated by tyrosine phosphorylation in response to epidermal growth factor and interleukin-6.";	
FT	DOMAIN 580 670	RT	Science 264:95-98(1994).	
FT	MOD_RES 705 705	RNA	[3]	
FT	VARSPIC 727 727	RP	SEQUENCE FROM N.A. (ISOFORM STAT3A).	
FT	VARSPIC 701 701	RC	SEQUENCE FROM N.A. (ISOFORM STAT3A).	
FT	VARIANT 32 32	RT	SEQUENCE=Brain;	
FT	CONFICT 548 548	RA	MEDLINE=9501415; PubMed=7523373;	
FT	CONFICT 561 561	RA	Raz R., Durbin J.E., Levy D.E.;	
FT	CONFICT 667 667	RA	/FTId=VAR_018683.	
FT	CONFICT 730 730	RA	/FTId=VAR_018679.	
FT	SEQUENCE 770 AA; 88067 MN; 6C00632211C8012D CRC64;	RA	Q -> H (in Ref. 1). P -> S (in Ref. 1). K -> N (in Ref. 1). F -> Y (in Ref. 1). V -> L (in Ref. 1).	
Best Local Similarity 99.2%; Score 1377; DB 1; Length 770; Matches 269; Conservative 1; Mismatches 1; Indels 0; Gaps 0; [2]	RN	W -> I. T -> A (in Ref. 1). M -> I.		
Query 1 RCLWEESRLQATAAQGCGNHPAAVTEKQMLHQDVEKRVQDLEQKMKVH 60	Qy	RT	"Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";	
Db 107 RCLWEESRLQATAAQGCGNHPAAVTEKQMLHQDVEKRVQDLEQKMKVH 166	Db	RT	J. Biol. Chem. 269:24391-24395(1994).	
Query 61 NIQDDDFNYKILKSGQDMQDINGNQNSVTRQKMQLEQMLTALDQMRRSIVSELAGLIS 120	Qy	RP	SEQUENCE FROM N.A. (ISOFORM STAT3B).	
Db 167 NLQDDDFNYKILKSGQDMQDINGNQNSVTRQKMQLEQMLTALDQMRRSIVSELAGLIS 226	Db	RC	SEQUENCE=BAIB/C, and C57BL/6; TISSUE=Liver;	
Query 121 AMEVYQKLTIBELADWKRREPIACTGGPPNCLDRLENWTLASBQLQQTKLKE 180	Qy	RA	Schaefer T.S., Sanders L.K., Nathans D.;	
Db 227 AMEVYQKLTIBELADWKRREPIACTGGPPNCLDRLENWTLASBQLQQTKLKE 286	Db	RT	"Cooperative transcriptional activity of Jun and Stat3 beta, a short form of Stat3";	
Query 181 LQQKVSKGDPVQHRPMLKSAFYTERQCPMPMPDRPLVTKTGQFT 240	Qy	RT	Proc. Natl. Acad. Sci. U.S.A. 92:9097-9101(1995).	
Db 287 LQQKVSKGDPVQHRPMLKSAFYTERQCPMPMPDRPLVTKTGQFT 346	Db	RL	[5]	
Query 241 TKURLVLFPEINYQKIKVCDKDSQDVA 271	Qy	RN	SEQUENCE FROM N.A. (ISOFORM STAT3A).	
Db 347 TKURLVLFPEINYQKIKVCDKDSQDVA 377	Db	RC	SEQUENCE FROM N.A. (ISOFORM STAT3A).	
RESULT 3		RC	SEQUENCE FROM N.A. (ISOFORM STAT3A).	
ID STA3_MOUSE STANDARD; PRT; 770 AA.		RX	SEQUENCE FROM N.A. (ISOFORM STAT3A).	
AC P42227;		RA	PubMed=1161803; DOI=10.1006/geno.2000.6433;	
DT 01-NOV-1995 (Rel. 32, Created)		RA	Miyoshi K., Cui Y., Riedlinger G., Robinson P., Lehoczyk J., Zon L., Oka T., Dewar K., Henninghausen L.;	
DT 01-OCT-1996 (Rel. 34, Last sequence update)		RA	"Structure of the mouse Stat3 3/5 locus: evolution from <i>Drosophila</i> to zebrafish to mouse.";	
DT 01-OCT-2004 (Rel. 45, Last annotation update)		RA	RT	[6]
DB Signal transducer and activator of transcription 3 (Acute-phase response factor).		RA	RT	"A mutant Stat3b with weaker DNA binding defines a key defective pathway in non-obese diabetic (NOD) mice.";
DE Name=Stat3; Synonyms=Aprf;		RA	RT	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
GN Mus musculus (Mouse);		RA	[7]	
OS Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		RP	SEQUENCE FROM N.A. (ISOFORM STAT3A).	
OC NCBI_TaxID=10090;		RC	SEQUENCE=FVB/N; TISSUE=Mammary gland;	
OX [1] SEQUENCE FROM N.A. (ISOFORM STAT3A), AND SEQUENCE OF 154-158; 181-185		RX	MEDLINE=2238827; PubMed=1247932; DOI=10.1073/pnas.242603899;	
RP AND 632-640.		RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marras M.A., Genration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";	
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RC MEDLINE=94120802; PubMed=7512451;		RN	[8]	
RX PHOSPHORYLATION SITE SER-727, AND NUTAGENESIS.		RA	PHOSPHORYLATION SITE SER-727, AND NUTAGENESIS.	
RA MEDLINE=95354205; PubMed=754024;		RX	MEDLINE=95354205; PubMed=754024;	
RA Wen Z., Zhong Z., Darnell J.E. Jr.; "Maximal activation of transcription by Stat1 and Stat3 requires both tyrosine and serine phosphorylation.";		RT	Cell 82:241-250(1995).	
RT Cell 77:63-71(1994).		RL	[9]	
RR X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.		RX	X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716.	
RR MEDLINE=98334373; PubMed=9671298;		RR	MEDLINE=98334373; PubMed=9671298;	

RA Becker S., Groner B., Mueller C.W.; "Three-dimensional structure of the Stat3beta homodimer bound to DNA." Nature 394:145-151(1998)

RT -!- FUNCTION: Transcription factor that binds to the interleukin-6 (IL-6)-responsive elements identified in the promoters of various acute-phase protein genes. STAT3B interacts with the N-terminal part of JUN to activate such promoters in a cooperative way.

CC -!- PATHWAY: Involved in the gp130-mediated signaling pathway.

CC -!- SUBUNIT: Forms a homodimer or a heterodimer with a related family member (at least STAT1) (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus in response to phosphorylation.

CC -!- ALTERNATIVE PRODUCTS:

Event: Alternative splicing; Named isoforms=3;

Name=Stat3A;

CC IsoId=p42227-1; Sequence=Displayed;

Name=Stat3B;

CC IsoId=p42227-2; Sequence=vsp_006287;

Name=Del-701;

CC IsoId=p42227-3; Sequence=vsp_010475;

CC -!- TISSUE SPECIFICITY: STAT3A is seen in the liver, spleen, and kidney. STAT3B is also detected in the liver, although in a much less abundant manner.

CC -!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNF, LIF, CSF-1, EGF, PDGF, IFN-alpha and OSM. Serine phosphorylation is important for the formation of stable DNA-binding STAT3 homodimers and maximal transcriptional activity (By similarity).

CC -!- SIMILARITY: Belongs to the transcription factor STAT family.

CC -!- SIMILARITY: Contains 1 SH2 domain.

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CC

DR EMBL; L29278; AAA37254.1; -.

DR EMBL; U05922; AAA19452.1; -.

DR EMBL; U08378; AA56688.1; -.

DR EMBL; U30709; AAC5212.1; -.

DR EMBL; AF246978; AAU59017.1; -.

DR EMBL; AY299489; AAQ15418.1; -.

DR EMBL; AY299490; AAQ15419.1; -.

DR EMBL; BC0033806; AAU033806.1; -.

DR PIR; 149508; 149508

DR PDB; 1BGI; X-ray; A=1-722.

DR TRANSFAC; T01574; -.

DR MGI; MGI-103039; Stat3.

DR GO; GO:0005537; C:cytoplasm; IDA.

DR GO; GO:0005634; C:nucleus; IDA.

DR GO; GO:0005886; C:plasma membrane; IDA.

DR GO; GO:003677; F:DNA binding; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0016563; F:transcriptional activator activity; IDA..

DR GO; GO:007259; P:JAK-STAT cascade; IDA.

DR GO; GO:0006357; P:regulation of transcription from Pol II pro .. ; IDA..

DR InterPro; IPR008967; P:regulation of transcription from Pol II pro .. ; IDA..

DR InterPro; IPR00980; SH2_3D-structure; Activator; Acute phase; Alternative splicing; Direct protein sequencing; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.

DR DOMAIN; DOMAIN; STAT_alpha_1.

DR Pfam; PF02864; STAT_bind_1.

DR Pfam; PF02865; STAT_int_1.

DR PROSITE; PS5001; SH2_1.

KW D-structure; Activator; Acute phase; Alternative splicing; Direct protein sequencing; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain; Transcription regulation.

FT DOMAIN; 580; 670; SH2.

FT MOD_RES; 705; 705; Phosphotyrosine (by JAK) (By similarity).

FT MOD_RES; 727; 727; Phosphoserine.

PT	VARSPLIC	716	770	TCNSNTIDLPMSPRTDSLMOFGNNCEGAEPPSAGCQFESLT FDMDLNSECATSPM -> FIDAVWK (in isoform Stat3B).
PT	MUTAGEN	727	727	/PTid=vsp_010475. Missing (in isoform Del-701). S->A: Decreased transcriptional activation.
PT	CONFICT	16	16	E -> K (in Ref. 2); S -> T (in Ref. 2 and 4).
PT	CONFFLICT	25	25	M -> I (in Ref. 1).
PT	TURN	139	180	PT HELIX
PT	TURN	181	182	PT TURN
PT	TURN	197	198	PT HELIX
PT	TURN	199	237	PT TURN
PT	TURN	238	238	PT HELIX
PT	TURN	252	253	PT HELIX
PT	TURN	261	290	PT TURN
PT	TURN	294	295	PT HELIX
PT	TURN	297	301	PT STRAND
PT	TURN	320	320	PT TURN
PT	STRAND	321	328	PT TURN
PT	STRAND	330	331	PT 333
PT	STRAND	335	337	PT TURN
PT	STRAND	338	340	PT STRAND
PT	STRAND	341	342	PT TURN
PT	STRAND	345	351	PT STRAND
Query	Best Local Similarity	99.2%	Score 1377; DB 1; Length 770;	
Query	Matches 269; Conservative	99.3%; Pred. No 2e-77; 1;	Mismatches 0; Indels 0; Gaps 0;	
Query	1 RCIWEESRLQTAATAQAOQSQANHPTAAVTEKOMLECHQDVKRVPDLEOKMKVVE	60	107 RCIWEESRLQTAATAQAOQSQANHPTAAVTEKOMLECHQDVKRVPDLEOKMKVVE	166
Db	61 NLQDDDPFYNYKTLKSQGDMDQLINGNMQSVIQRQKQMLEQMTALDMQRSSVSELAGLS	120	61 NLQDDDPFYNYKTLKSQGDMDQLINGNMQSVIQRQKQMLEQMTALDMQRSSVSELAGLS	226
Db	167 NLQDDDPFYNYKTLKSQGDMDQLINGNMQSVIQRQKQMLEQMTALDMQRSSVSELAGLS	226	121 AMEVYVQTLTDEELADWKRRPEIACTGGPPNCLDRLENWITSLAESQLQTROQIKLEE	180
Db	227 AMEVYVQTLTDEELADWKRRQIACTGGPPNCLDRLENWITSLAESQLQTROQIKLEE	286	227 AMEVYVQTLTDEELADWKRRQIACTGGPPNCLDRLENWITSLAESQLQTROQIKLEE	286
Query	181 LQQKSYKGPDIIVQRPMPLERIVELFLRNKSAFVERPQCPMPMPDRPVIKTGQFT	240	181 LQQKSYKGPDIIVQRPMPLERIVELFLRNKSAFVERPQCPMPMPDRPVIKTGQFT	240
Db	287 LQQKSYKGPDIIVQRPMPLERIVELFLRNKSAFVERPQCPMPMPDRPVIKTGQFT	346	287 LQQKSYKGPDIIVQRPMPLERIVELFLRNKSAFVERPQCPMPMPDRPVIKTGQFT	346
Query	241 TKURLVKEPELYNOLKIKYCIDKSGDVA	271	241 TKURLVKEPELYNOLKIKYCIDKSGDVA	271
Db	347 TKVRLLVKEPELYNOLKIKYCIDKSGDVA	377	347 TKVRLLVKEPELYNOLKIKYCIDKSGDVA	377
RESULT 4	STAS3_RAT			
ID	STAS3_RAT	STANDARD;	PRT;	770 AA.
AC	P52631;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Signal transducer and activator of transcription 3.			
GN	Name=Stat3;			
OS	Rattus norvegicus (Rat).			
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Olfactores; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBII_TAXID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	MEDLINE=96102059; PubMed=8530402; Ripperger J.A., Fritz S., Richter K., Hocke G.M., Lottspeich F.,			

RA RA
 RT "Transcription factors Stat3 and Stat5b are present in rat liver
 nucle late in an acute phase response and bind interleukin-6 response
 elements";
 J. Biol. Chem. 270:29998-30005(1995).

-!- FUNCTION: Transcription factor that binds to the interleukin-6
 (IL-6)-responsive elements identified in the promoters of various
 acute phase protein genes.

-!- PATHWAY: Involved in the gp130-mediated signaling pathway.

-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 member (at least STAT1) (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 in response to phosphorylation (By similarity).

-!- PTM: Tyrosine phosphorylated in response to IL-6, IL-11, CNTF,
 LIF, CSF-1, EGF, PDGF, TN-alpha and OSM. Serine phosphorylation
 is important for the formation of stable DNA-binding STAT3
 homodimers and maximal transcriptional activity (By similarity).

-!- SIMILARITY: Belongs to the transcription factor STAT family.

-!- SIMILARITY: Contains 1 SH2 domain.

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EMBL: X98110; CAA6920.1; -.
 DR HSSP; P42227; IBGI.
 DR RGB; 3772; Stat3.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR Pfam; PF00017; SH2_1.
 DR Pfam; PF01017; STAT_alpha_1.
 DR Pfam; PF22864; STAT_bind_1.
 DR Pfam; PF22865; STAT_int_1.
 DR SMART; SM00252; SH2_1.
 PROSITE; PS50001; SH2_1.
 KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
 KW Transcription regulation.

Best local Similarity 98.9%; Score 1374; DB 1; Length 770;
 Matches 268; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RCLWERSRLQATAAQCGQOANHPTAAYTEKQOMLEQHQDTRKRVQDLEQKMKVVE 60
 Db 107 RCLWERSRLQATAAQCGQOANHPTAAYTEKQOMLEQHQDTRKRVQDLEQKMKVVE 166

QY 61 NLQDDDFPNKTKLKSQGMDQDLINGNQSVTRQMKQLEOMLTALDQMRSSIVSELAGLIS 120
 167 NLQDDDFPNKTKLKSQGMDQDLINGNQSVTRQMKQLEOMLTALDQMRSSIVSELAGLIS 226

QY 121 AMEYVQKTLDEELADWKRRPEIACGGPPNCLDRLENNTSLAESQLTROQQKKLEE 180
 227 AMEYVQKTLDEELADWKRRPEIACGGPPNCLDRLENNTSLAESQLTROQQKKLEE 286

QY 181 LQOKYSYKGDPIVQHRPMLESERIVFLRNLMKSAFVVERCPMPMPDRDLVIKGQVFT 240
 287 LQOKYSYKGDPIVQHRPMLESERIVFLRNLMKSAFVVERCPMPMPDRDLVIKGQVFT 346

QY 241 TKVRLIVKPEPELYQIKIVCIDKQSGDVA 271
 347 TKVRLIVKPEPELYQIKIVCIDKQSGDVA 377

STA3_BOVIN ID STA3_BOVIN STANDARD; PRT: 770 AA.
 AC P61635; DT 05-JUL-2004 (Rel. 44, created)
 CC DT 05-JUL-2004 (Rel. 44, last sequence update)
 CC DT 01-OCT-2004 (Rel. 45, last annotation update)
 DE Signal transducer and activator of transcription 3.
 GN Name=STAT3;
 OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Pecora; Bovidae;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1] -
 RP TISSUE=Mammary gland;
 RA "The STAT5B-encoding gene was flipped across the STAT3/STAT5A-locus
 during ruminant evolution.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Transcription factor that binds to the interleukin-6
 (IL-6)-responsive elements identified in the promoters of various
 acute phase protein genes (By similarity).

-!- PATHWAY: Involved in the gp130-mediated signaling pathway.

-!- SUBUNIT: Forms a homodimer or a heterodimer with a related family
 member (at least STAT1) (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic; translocated into the nucleus
 in response to phosphorylation (By similarity).

-!- SIMILARITY: Belongs to the transcription factor STAT family.

-!- SIMILARITY: Contains 1 SH2 domain.

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 or send an email to license@sb-sib.ch).

CC DR EMBL; AJ220655; CAA06182.1; -.
 CC DR PROSITE; PS50001; SH2_1.
 CC KW Activator; DNA-binding; Nuclear protein; Phosphorylation; SH2 domain;
 KW Transcription regulation.

FT DOMAIN 580 670 SH2.
 FT MOD RES 705 705 Phosphotyrosine (by JAK) (By similarity).
 FT SEQUENCE 770 AA; 88039 MW; D74A0C76954754ED CRC64;

Query Match 98.7%; Score 1370; DB 1; Length 770;
 Best Local Similarity 98.9%; Pred. No. 5.3e-77; 2; Indels 0; Gaps 0;
 Matches 268; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RCLWERSRLQATAAQCGQOANHPTAAYTEKQOMLEQHQDTRKRVQDLEQKMKVVE 60
 Db 107 RCLWERSRLQATAAQCGQOANHPTAAYTEKQOMLEQHQDTRKRVQDLEQKMKVVE 166

QY 61 NLQDDDFPNKTKLKSQGMDQDLINGNQSVTRQMKQLEOMLTALDQMRSSIVSELAGLIS 120
 167 NLQDDDFPNKTKLKSQGMDQDLINGNQSVTRQMKQLEOMLTALDQMRSSIVSELAGLIS 226

Db 121 AMEYVQKTLDEELADWKRRPEIACGGPPNCLDRLENNTSLAESQLTROQQKKLEE 180
 227 AMEYVQKTLDEELADWKRRPEIACGGPPNCLDRLENNTSLAESQLTROQQKKLEE 286

QY 181 LQOKYSYKGDPIVQHRPMLESERIVFLRNLMKSAFVVERCPMPMPDRDLVIKGQVFT 240
 287 LQOKYSYKGDPIVQHRPMLESERIVFLRNLMKSAFVVERCPMPMPDRDLVIKGQVFT 346

Db 241 TKVRLIVKPEPELYQIKIVCIDKQSGDVA 271
 QY 347 TKVRLIVKPEPELYQIKIVCIDKQSGDVA 377

RESULT 6	Q6UV79	PRELIMINARY;	PRT;	771 AA.
	Q6DV79;			
	Q6DV79;			
	01-OCT-2004 (TREMBrel. 28, Last sequence update)			
	01-OCT-2004 (TREMBrel. 28, Last annotation update)			
DE	Signal transducer and activator of transcription 3.			
DR	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OX	NBIL_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zhou G.Y.; Leung F.C.;			
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AV641397; AAT64897.1; -.			
SQ	SEQUENCE 771 AA; 88174 MW; 71AC855C5DEC03E2 CRC64;			
Query Match	Best local similarity 97.4%; Score 1352; DB 2; Length 771; Matches 264; Conservative 1; Mismatches 6; Indels 0; Gaps 0;			
QY	1 RCLMEFESRLQIATAAQGQANHPTAAVTEQKQLEHQFLQWRKVQDLEQMKVVE 60			
Db	107 RCLMEFESRLQIATAAQGQANHPTAAVTEQKQLEHQFLQWRKVQDLEQMKVVE 60			
QY	61 NLQDDDFENYKTKLSQGDMDLNGNQNSYTRQKQOLEMTALIQMRNISIVSAGLIS 120			
Db	167 NLQDDDFENYKTKLSQGDMDLNGNQNSYTRQKQOLEMTALIQMRNISIVSAGLIS 120			
QY	121 AMEYVQKLTDEELADWKRRPEIAGIGGPNCIDRLENWITSLAESQIQTQQIKKLEE 180			
Db	227 AMEYVQKLTDEELADWKRRPEIAGIGGPNCIDRLENWITSLAESQIQTQQIKKLEE 180			
QY	181 LQOKVSYKGDPIVQHRPMLEERIVELFRNLMSAVERQPQCMMPHPDRPLVIKGQFT 240			
Db	287 LQOKVSYKGDPIVQHRPMLEERIVELFRNLMSAVERQPQCMMPHPDRPLVIKGQFT 240			
QY	241 TKVRLLVKRPELNTQLKIKVCKIDKSGDVA 271			
Db	347 TKVRLLVKRPELNTQLKIKVCKIDKSGDVA 271			
RESULT 7				
Q9PVX8	PRELIMINARY;	PRT;	769 AA.	
AC	Q9PVX8;			
DT	01-MAY-2000 (TREMBrel. 13, Created)			
DT	01-MAR-2004 (TREMBrel. 13, Last sequence update)			
DE	Stat 3.			
GN	Name=stat 3;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.			
OC	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RX	MEDLINE=20107399; PubMed=1642787;			
RA	Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.; Schueler G.D.,			
RA	Klausner R.D.; Collins F.S.; Wagner L.; Shemmen C.M.; Alischul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bnat N.K.,			
RA	Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.,			
RA	Ditschenko L.; Marusina K.; Farmer A.A.; Robin G.M.; Hong L.; Stapleton M.; Soakes M.B.; Bonaldo M.F.; Cabant T.L.; Scheetz T.E.,			
RA	Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.,			
RA	Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mulhaby S.J.,			
RA	Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Guarante P.H.,			
RA	Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.,			
RA	Villalon D.K.; Munney D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.,			
RA	Fahay J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.,			
RA	Whiting M.; Madan A.; Young A.C.; Sherchenko Y.; Bouffard G.G.,			
RA	Blaesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.,			
RA	Rodriguez A.C.; Grimwood J.; Schmitz J.; Myers R.M.; Butterfield Y.S.,			
RA	Jones S.J.; Marra M.A.; Skalska U.; Smailus D.E.; Schnurch A.; Schein J.E.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			

RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontus J., Clifton S.W.,
 Richardson P.; "Genomic tools for Xenopus research: The NIH Xenopus
 initiative"; Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC044717; AAH4717.1;
 GO; GO:0005634; C:nucleus; IEA.
 GO; GO:0004871; F:signal transducer activity; IEA.
 GO; GO:0003700; F:transcription factor activity; IEA.
 GO; GO:0007242; P:intracellular signaling cascade; IEA.
 GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 PFam; PF00017; SH2; 1.
 DR Pfam; PF02864; STAT_bird; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR SEQUENCE 766 AA; 87599 MW; 31018A3321CCEB9C CRC64;
 Query Match 92.7%; Score 1286; DB 2; Length 766;
 Best Local Similarity 91.1%; Pred. No. 8.9e-72;
 Matches 247; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
 QY 1 RCLWEESRLQTAATAQCGGQANHTAAVTEKQMLQHQDVKRVDQLEOKKVVS 60
 Db 107 RCLWEERGLQTAATAQCGGQASHENAAVITEKQMLQHQDVKRVDQLEOKKVVS 166
 QY 61 NLQDDDFNYKTLKSQDLMQDLANGNNSVTRQKMQOLEQMTALDQMRSSIVSELAGLLS 120
 Db 167 NLQDDDFNYKTLKSQDLMQDLANGNNSVTRQKMQOLEQMTALDQMRSSIVSELAGLLS 226
 QY 121 AMEVYVKTILDEELAKWKRREPIACTGGPPNCLDLENWITSLASLQSOLTRQQIKLES 180
 Db 227 AMEVYVKTILDEELAKWKRREPIACTGGPPNCLDLENWITSLASLQSOLTRQQIKLES 286
 Qy 181 LQQKVSYKDPPIQHRPMLEERIVELFRNLIMSAFVERQPCMPMPDRPLVIKGQFT 240
 Db 287 LQQKVSYKDPPIQHRPMLEERIVELFRNLIMSAFVERQPCMPMPDRPLVIKGQFT 346
 QY 241 TKVRLVLPKPELNQYQIKIKVCIKDSDVAA 271
 Db 347 NKVRLVLPKPELNQYQIKIKVCIKDSDGAA 377
 RESULT 9
 Q7TSS PRELIMINARY; PRT; 414 AA.
 AC Q7TSS;
 DT 01-JUN-2003 (TREMBrel. 24, Created)
 DT 01-JUN-2003 (TREMBrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 DR stat3 protein.
 GN Name=stat3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio;
 OC NCBI_TaxID=7955;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Hsieh F.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Blueton K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoieh F.,
 RA Diatchenko L., Marszina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., MEBIAN P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Keittman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 DR Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC045276; AAH45276.1;
 DR ZFIN; ZDB-GENE:980026-68; stat3.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR001217; STAT.
 PFam; PF00017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR Pfam; PF02865; STAT_int; 1.
 DR SEQUENCE 414 AA; 48253 MW; OFPD1B509B7526BD CRC64;
 Query Match 85.8%; Score 1191.5; DB 2; Length 414;
 Best Local Similarity 84.6%; Pred. No. 3.3e-66;
 Matches 231; Conservative 22; Mismatches 3; Indels 3; Gaps 3;
 QY 1 RCLWEESRLQTAATAQCGGQANHTAAVTEKQMLQHQDVKRVDQLEOKKVVE 60
 Db 107 RCLWEERGLQTAATAQCGGQAVRPTGTGVTVTEKQMLQHQDVKRVDQLEOKKVVE 165
 QY 61 NLQDDDFNYKTLKSQDLMQDLANGNNSVTRQKMQOLEQMTALDQMRSSIVSELAGLLS 118
 Db 166 NLQDDDFNYKTLKSQDLMQDLANGNNSVTRQKMQOLEQMTALDQMRSSIVSELAGLLS 225
 QY 119 LSAAMEVYVKTILDEELAKWKRREPIACTGGPPNCLDLENWITSLASLQSOLTRQQIKLS 178
 Db 226 LSAMDEVYVKTILDEELAKWKRREPIACTGGPPNCLDLENWITSLASLQSOLTRQQIKLS 285
 QY 179 EELQQKVSYKDPPIQHRPMLEERIVELFRNLIMSAFVERQPCMPMPDRPLVIKGQ 238
 Db 286 EELQQKVSYKDPPIQHRPMLEERIVELFRNLIMSAFVERQPCMPMPDRPLVIKGQ 345
 QY 239 FITKVLVLPKPELNQYQIKIKVCIKDSDGAA 271
 AC 06NV46
 ID 06NV46;
 AC 06NV46;
 DT 05-JUL-2004 (TREMBrel. 27, Created)
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)

DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	RESULT 11
DR	Stat3 protein.	AHH68320
GN	Name=stat3;	ID AHH68320 PRELIMINARY; PRT; 786 AA.
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	AC AHH68320;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	DT 10-MAY-2004 (TREMBLrel. 27, Created)
CC	Cyprinidae; Danio.	DT 10-MAY-2004 (TREMBLrel. 27, Last sequence update)
OX	NCBI_TaxID=7955;	DE Stat3 protein.
RN	[1]	GN STAT3.
RP	SEQUENCE FROM N.A.	OS Brachydanio rerio (zebrafish) (Danio rerio).
RC	TISSUE=Kidney;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
RX	MEDLINE=2288257; PubMed=12477932;	OC Cyprinidae; Danio.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schenck C.M., Schuler G.D.,	OC
RA	Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schaefer C.F., Bhat N.K.,	OC
RA	Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	OX NCBI_TaxID=7955;
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	RN [1]
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	RP SEQUENCE FROM N.A.
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,	RC TISSUE=Kidney;
RA	Brownstein M.J., Usdin T.B., Toshikuni S., Carninci P., Prange C.,	RX MEDLINE=2288257; PubMed=12477932;
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	RA Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Fahay J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,	RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	RA Brownstein M.J., Usdin T.B., Toshikuni S., Carninci P., Prange C.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	[1]	RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Jones S.J., Marra M.A.;	RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RT	"Generation and initial analysis of more than 15,000 full-length human	RA Fahay J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RT	and mouse cDNA sequences";	RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RT	proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RL	SEQUENCE FROM N.A.	RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RR		RA [1]
RC	TISSUE=Kidney;	RA Krzywinski M.I., Skalska U., Smialius D.E., Schnurch A., Schein J.E.,
RA	Strasberg R.;	RA Jones S.J., Marra M.A.;
RL	Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.	RT "Generation and initial analysis of more than 15,000 full-length human
DR	EMBL; BC058320; AAH68320_1; -.	RT and mouse cDNA sequences";
DR	IntePro; IPR008967; P53_like_DNA_bnd.	RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
DR	InterPro; IPR00980; SH2.	RN [2]
DR	InterPro; IPR001217; STAT.	RP SEQUENCE FROM N.A..
DR	PF00017; SH2; 1.	RC TISSUE=Kidney;
DR	PFam; PF01017; STAT_alpha; 1.	RA Strasberg R.,
DR	PFam; PF02864; STAT_bind; 1.	RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR	PROSITE; PS50001; SH2; 1.	DR EMBL; BC058320; AAH68320_1; -.
DR	SEQUENCE; PS50001; SH2; 1.	DR SEQUENCE 786 AA;, 90039 MW; FC7371D0B0E5447E CRC64;
SQ	Query Match 85.8%; Score 1191.5; DB 2; Length 786; Best Local Similarity 84.6%; Fred. No. 6.8e-16; Matches 231; Conservative 22; Mismatches 17; Indels 3; Gaps 3; Query 1 RCLWEESSLQIQTATAAQGSGQANHPTAVVTEKQMLEHQIDQVRKVDDLRKRVVE 60	Query Match 85.8%; Score 1191.5; DB 2; Length 786; Best Local Similarity 84.6%; Fred. No. 6.8e-16; Matches 231; Conservative 22; Mismatches 17; Indels 3; Gaps 3; Query 1 RCLWEESSLQIQTATAAQGSGQANHPTAVVTEKQMLEHQIDQVRKVDDLRKRVVE 60
QY	107 RCLWEESSLQIQTATAAQGSGQANHPTAVVTEKQMLEHQIDQVRKVDDLRKRVVE 60	QY 107 RCLWEESSLQIQTATAAQGSGQANHPTAVVTEKQMLEHQIDQVRKVDDLRKRVVE 60
Db	61 NLQDDDFNYKTKLSQGDM-QDINGNGO-SVTROKMQOLMTALDOMRSIVTELAGL 118	Db 107 RCLWEESSLQIQTATAAQGSGQANHPTAVVTEKQMLEHQIDQVRKVDDLRKRVVE 60
QY	166 NLQDDDFNYKTKLSQGELSDQDINGNSQAAATROKMSQLEQMSALDQLRQQIVIEWAGL 225	QY 61 NLQDDDFNYKTKLSQGDM-QDINGNGO-SVTROKMQOLMTALDOMRSIVTELAGL 118
Db	119 LSAMEVYQKLTDEELADWKRPKEFACIGGPNCIDRLEWITSLAESQLOTRQOKKL 178	Db 166 NLQDDDFNYKTKLSQGELSDQDINGNSQAAATROKMSQLEQMSALDQLRQQIVIEWAGL 225
QY	226 LSAMDVFVQNLTEELADWKRPKEFACIGGPNCIDRLEWITSLAESQLOTRQOKKL 285	QY 119 LSAMEVYQKLTDEELADWKRPKEFACIGGPNCIDRLEWITSLAESQLOTRQOKKL 178
Db	179 BELQOKVISYKGDPIVQHRPMLERIVELFLRNLMSKAFAVVERQPCMPMHPDRPLVKTGVQ 238	Db 226 LSAMDVFVQNLTEELADWKRPKEFACIGGPNCIDRLEWITSLAESQLOTRQOKKL 285
QY	286 BELQOKVISYKGDPIVQHRPMLERIVELFLRNLMSKAFAVVERQPCMPMHPDRPLVKTGVQ 345	QY 179 BELQOKVISYKGDPIVQHRPMLERIVELFLRNLMSKAFAVVERQPCMPMHPDRPLVKTGVQ 238
Db	239 FTTKVRLLVKEPELNYQLKIKVCKIDKGSDGVAA 271	Db 286 BELQOKVISYKGDPIVQHRPMLERIVELFLRNLMSKAFAVVERQPCMPMHPDRPLVKTGVQ 345
QY	346 FTTKVRLLVKEPELNYQLKIKVCKIDKGSDGVAA 378	QY 239 FTTKVRLLVKEPELNYQLKIKVCKIDKGSDGVAA 271
Db		Db 346 FTTKVRLLVKEPELNYQLKIKVCKIDKGSDGVAA 378
		RESULT 12
		093599

AC	Q93599; Q93599;	PRELIMINARY; PRT; 806 AA.
DT	01-NOV-1998 (TREMBLrel. 03, Last sequence update)	
DT	01-NOV-1998 (TREMBLrel. 03, Last sequence update)	
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	
DE	Transcription factor.	
GN	Name=stat3;	
OS	Bacchocydio rerio (zebrafish) (Danio rerio).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	
OC	NCBI_TaxID=7955;	
RN	[1] SEQUENCE FROM N.A.	
RA	Ostee A.C.; Thesis (1998), University of Melbourne, Australia.	
RL	RL Liu R., Hong Y.;	
DR	DR Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.	
DR	DR EMBL; AY641434; AAT46364; 1; -.	
ZFIM	ZDB-GENE-980526-68; stat3.	
DR	DR GO; GO:000534; C:nucleus; IEA.	
DR	DR GO; GO:0003700; F:transducer activity; activity; IEA.	
DR	DR GO; GO:0007142; P:intercellular signaling cascade; IEA.	
DR	DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR	DR InterPro; IPR008967; P53_like_DNA_bnd.	
DR	DR InterPro; IPR001217; STAT.	
DR	DR Pfam; PF00017; SH2; 1.	
DR	DR Pfam; PF01017; STAT alpha; 1.	
DR	DR Pfam; PF02864; STAT bind; 1.	
DR	DR Pfam; PF02865; STAT_int; 1.	
DR	DR SMART; SW0052; SH2; 1.	
DR	DR PROSITE; PS00001; SH2; 1.	
SQ	SEQUENCE 806 AA; 92151 MW; 74BC4EA401C3C942 CRC64;	
Query Match	Best Local Similarity 85.8%; Score 1191.5; DB 2; Length 806;	
Matches	231; Conservative 84.6%; Pred. No. 7e-66; Mismatches 17; Indels 3; Gaps 3;	
QY	1 RCLWEERSRILQQTAAQAQGQQANHPTAAVTEKQOMLEQHQIQRKVQDLEQMKVVE 60	
Db	107 RCLWEEQRLLQT-ATTAQDGQVAHPTGTIVTEKQLEHNLDQDIRKRVQDMEQKOMLE 165	
QY	61 NLQDDDFENYTKLSQGDM-OQDNGNNO-SVTROKQQLQEMQMLTDOMERSVSLAGL 118	
Db	226 LTAMDYVQRNLTDDEBLADWKRRQQTACIGGFPNCLDIRLRTWTISLAESOLQIRQQIKKL 285	
QY	179 FELOQKVSYKGDPVQHRPMLEEVLFNLMSAFVVERQPQCPMPHPDRPLVIKTGVQ 238	
Db	286 FELOQKVSYKGDPVQHRPALEKTVDFLNLMKSAFVVERQPQCPMPHPDRPLVIKTGVQ 345	
QY	239 FTTKVRLLVKEPELYNQLKVKVCDKDSGDVA 271	
Db	346 FTNKURLLVKEPELYNQLKVKVCDKESGVAA 378	
RESULT 14		
Q6GU87	Q6GU87 PRELIMINARY; PRT; 785 AA.	
ID	ID 06GU87	
AC	AC 06GU87	
DT	DT 05-JUL-2004 (TREMBLrel. 27, Created)	
DT	DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DR	DR Signal transducer and activator of transcription 3 isoform 1.	
OS	OS Oryzias latipes (Medaka fish) (Japanese ricefish).	
OC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	
OC	OC Acanthopterygii; Percormorpha; Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.	
OC	OC NCBI_TaxID=8090;	
RN	[1] SEQUENCE FROM N.A.	
RA	RA Liu R., Hong Y.;	
RL	RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.	
DR	DR EMBL; AY641434; AAT46364; 1; -.	
DR	DR InterPro; IPR008967; P53_like_DNA_bnd.	
DR	DR InterPro; IPR000980; SH2.	
DR	DR Pfam; PF00017; SH2; 1.	
DR	DR Pfam; PF01017; STAT alpha; 1.	
DR	DR Pfam; PF02864; STAT_bind; 1.	
DR	DR Pfam; PF02865; STAT_int; 1.	
DR	DR PROSITE; PS00001; SH2; 1.	
SQ	SEQUENCE 785 AA; 89643 MW; 81F231BDE27DB938 CRC64;	
Query Match	Best Local Similarity 85.2%; Score 1182.5; DB 2; Length 785;	
Matches	229; Conservative 83.9%; Pred. No. 2.5e-65; Mismatches 19; Indels 3; Gaps 3;	
QY	1 RCLWEERSRILQQTAAQAQGQQANHPTAAVTEKQOMLEQHQIQRKVQDLEQMKVVE 60	
Db	107 RCLWEEQRLLQT-ATTAQDGQVAHPTGTIVTEKQLEHNLDQDIRKRVQDMEQKOMLE 165	
QY	61 NLQDDDFENYTKLSQGDM-OQDNGNNO-SVTROKQQLQEMQMLTDOMERSVSLAGL 118	
Db	166 NLQDDDFENYTKLSQGEMQMLTDOMERSVSLAGL 225	

Qy 119 LSAMEYVQKLTDEELADWKRRPEIACIGGPPNCLDRLENWTSLASLQSQTROQIKKL 178
 Db 226 ITAMDVYQKNLDEELADWKRRQQIACTIGGPPNCLDRLENWTSLASLQSQTROQIKKL 285

Qy 179 EELQOKSYKGPIVQRPMLTERTIVELFRNAMSATVERQPCMPMPHDPRLVIKGQ 238
 Db 286 EELQOKSYKGPIQHRPALESEKIVDLFRNAMSATVERQPCMPMPHDPRLVIKGQ 345

Qy 239 FTKVRLVKEFELNYDKTKCIDSQGDVA 271
 Db 346 FTKVRLVKEFELNYDKTKCIDSQGDVA 378

RESULT 15

Q90Y16 PRELIMINARY; PRT; 764 AA.
 ID Q90Y16;
 AC ;
 DT 01-DEC-2001 (TREMBL; 19, Created);
 DT 01-DEC-2001 (TREMBL; 19, Last sequence update)
 DB STAT3.
 OS Tetradon fluviatilis (Puffer fish);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodon.
 OX NCBI_TaxId=47145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sung S.C., Fan T.J., Ieu J.H., Chou C.M., Huang C.J.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF307106; AAL09415.1; -;
 DR HSSP: P42227; IBGI.
 DR GO: GO:0005634; C:nucleus; IEA:
 DR GO: GO:0004871; F:signal transducer activity; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0007242; P:interracellular signaling cascade; IEA.
 DR InterPro; IPR008967; P53_like_DNA_bnd.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001217; STAT.
 DR PFam; PF00017; SH2; 1.
 DR PFam; PF01017; STAT_alpha; 1.
 DR Pfam; PF02864; STAT_bind; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS5001; SH2; 1.
 SQ SEQUENCE 764 AA; 8741 MW; E661FFE18BEFD8BE CRC64;

Query Match 84.0%; Score 1165.5; DB 2; Length 764;
 Best Local Similarity 83.2%; Pred. No. 2.7e-64;
 Matches 227; Conservative 24; Mismatches 19; Indels 3; Gaps 3;

Qy 1 RCLWERSRLLQTTATAAQCGGCGANHTTAATVTEKKOQMLEHQDVKRVQDLEQKMKVE 60
 Db 107 RCLWERSRLLQTTATAAQCGGCGANHTTAATVTEKKOQMLEHQDVKRVQDLEQKMKVE 165

Qy 61 NLQDDDFPNYKTKSQQDM-QDINGNNO-SVTQRQKMQLEOMTALDQMRSSIVSBLAGL 118
 Db 166 NLQDDDFPNYKTKSQQDM-QDINGNNO-SVTQRQKMQLEOMTALDQMRSSIVSBLAGL 225

Qy 119 LSAMEYVQKLTDEELADWKRRPEIACIGGPPNCLDRLENWTSLASLQSQTROQIKKL 178
 Db 226 LTAMDVYQKNLDEELADWKRRQQIACTIGGPPNCLDRLENWTSLASLQSQTROQIKKL 285

Qy 179 EELQOKSYKGPIVQRPMLTERTIVELFRNAMSATVERQPCMPMPHDPRLVIKGQ 238
 Db 286 EELQOKSYKGPIQHRPALESEKIVDLFRNAMSATVERQPCMPMPHDPRLVIKGQ 345

Qy 239 FTKVRLVKEFELNYDKTKCIDSQGDVA 271
 Db 346 FTKVRLVKEFELNYDKTKCIDSQGDVA 378

Search completed: December 2, 2004, 23:52:25
 Job time : 196 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2004, 23:38:03 ; Search time 39 Seconds
 (without alignments)
 668.583 Million cell updates/sec

Title: US-10-090-185-9
 Perfect score: 1388
 Sequence: 1 RCLWERSRLQIATAAQCG.....LNQQLKIKV CIDKDSQDVAA 271
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query	Match Length	DB ID	Description
1	1377	99.2	770	2	I4950B ISGF3 p91-related transcription factor - mouse
2	1372	98.8	770	2	A54444 DNA-binding protein, interferon-dependent gamma-interferon alpha-1
3	601.5	43.3	739	2	A546159 interferon-gamma
4	582.5	42.0	748	2	A56047 interferon alpha-1
5	363.4	26.2	851	2	A46160 interferon-gamma
6	288.5	20.8	786	2	A49274 mammary gland fact
7	284.5	20.5	793	2	A54772 mammary gland fact
8	277.5	20.0	794	2	A62317 transcription activator
9	252.5	18.2	55527		mammary gland fact
10	122.9	9.3	837	2	A157557 DNA-Binding Protein
11	122.9	9.3	848	2	A54740 interleukin-4-indu
12	122.6	9.2	1208	2	A19147 chromosome segregat
13	122.6	9.1	978	2	A70387 conserved hypochet
14	125.5	9.0	1166	2	A27075 hypothetical prote
15	125.5	9.0	464	2	B19279 microtubule bindin
16	122.4	8.9	533	2	A272593 hypothetical prote
17	122.5	8.8	857	2	S33821 median body protei
18	122.5	8.8	1972	1	A41604 myosin heavy chain
19	120.0	8.6	734	2	A727055 hypothetical prote
20	120.0	8.6	1509	1	A27224 myosin heavy chain
21	118.5	8.5	2207	1	A506117 myosin heavy chain
22	118.5	8.5	2094	2	S33124 tpr protein - huma
23	118.8	8.5	284	2	A64527 M protein - Helico
24	118.8	8.5	2253	2	C64527 nuclear/mitotic ap
25	118.8	8.5	2442	2	T08621 centrosome associa
26	117.5	8.5	2007	1	B13402 myosin heavy chain
27	117.7	8.4	1807	1	S73852 hypothetical prote
28	117.7	8.4	1938	2	JC5421 smooth muscle myos
29	8.4		1972	2	JC5420 smooth muscle myos

RESULT 1

I4950B ISGF3 p91-related transcription factor - mouse

C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I4950B; I49009
 R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsuoka, T.; Yoshida, K.; Su Cell 77, 63-71, 1994
 A;Title: Molecular cloning of APRE, a novel IFN-stimulated gene factor 3 p91-related tr
 A;Reference: A54444; MUID:94208062; PMID:7512451
 A;Accession: I4950B
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Cross-references: UNIPROT:P42227; GB:L29278; NID:9476715; PID:AAA37254.1; PID:947671
 R;Raz, R.; Durbin, J.E.; Levy, D.E.
 J; Biol. Chem. 269, 2431-2435, 1994
 A;Title: Acute phase response factor and additional members of the interferon-stimulate
 A;Reference number: I49009; MUID:95014185; PMID:7523373
 A;Accession: I49009
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Cross-references: EMBL:U08378; NID:9473889; PID:AAA56668.1; PID:9473890
 C;Genetics:
 C;Amino acid sequence:
 C;Superfamily: human signal transducer and transcription activator STAT5A
 Query Match 99.2%; Score 1377; DB 2; Length 770;
 Best Local Similarity 99.3%; Pred. No. 4.8e-81; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 269; Conservative 1; Sbjct_start 1; Sbjct_end 770
 QY 1 RCLWERSRLQIATAAQCGQANHPTAVTKEQMLHQDVRKRYQVDQLEQKMKVE 60
 Db 107 RCLWERSRLQIATAAQCGQANHPTAVTKEQMLHQDVRKRYQVDQLEQKMKVE 166
 QY 61 NLQDDDFNYKTKLGSQGMDQDMDQDINGNNNQSVTQRMQOQLEQMLTAJDQMRSSIVSELAGLIS 120
 Db 167 NLQDDDFNYKTKLGSQGMDQDMDQDINGNNNQSVTQRMQOQLEQMLTAJDQMRSSIVSELAGLIS 226
 QY 121 AMEYVQXTLDELAQKWRPEIACGGPPNCLDRLENWITSLAESQLOTRQIKLEE 180
 Db 227 AMEYVQXTLDELAQKWRQOACTGGPPNCLDRLENWITSLAESQLOTRQIKLEE 286
 QY 181 LQQKSYKGPPIVQHRPMLERIVILFRNLMSAFVTPVERCPMPMPDPPLIVKQVFT 240
 Db 287 LQQKSYKGPPIVQHRPMLERIVILFRNLMSAFVTPVERCPMPMPDPPLIVKQVFT 346
 QY 241 TKVRLVKFPELNYQKIKV CIDKDSQDVAA 271
 Db 347 TKVRLVKFPELNYQKIKV CIDKDSQDVAA 377

RESULT 2

A54444 DNA binding protein APRF - human
 C;Species: Homo sapiens (man)
 C;Accession: A54444
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 R;Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.; Sud
 Cell, 77, 63-71, 1994
 A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related tra
 A;Reference number: A54444; MUID:94208062; PMID:7512451
 A;Accession: A54444
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-770 <RES>
 A;Cross-references: UNIPROT:P40763; GB:129277; NID:9475788; PID:9475789
 C;Genetics:
 A;Gene: GDB:STAT3; ARF
 A;Cross-references: GDB:358950
 A;Map position: 17q21-17q21
 C;Superfamily: human signal transducer and transcription activator STAT5A
 C;Keywords: DNA binding; transcription factor

Query Match 98.8%; Score 1372; DB 2; Length 770;
 Best Local Similarity 98.9%; Pred. No. 1e-80; Matches 268; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 1 RCLWERSRLQIATATAQGGQANHPTAAVTEKQOMLEQHLDQYKRVQDLEQMKVVE 60
 Qy 61 NLQDDDFNYKTKLKSQGDMQDINGNNQSVRQKQMLEQMLTDQMRSSVLSAQGQAHNTAAVTEKQOMLEQHLDQYKRVQDLEQMKVVE 166
 Db 107 RCLWERSRLQIATATAQGGQANHPTAAVTEKQOMLEQHLDQYKRVQDLEQMKVVE 60
 Qy 167 NLQDDDFNYKTKLKSQGDMQDINGNNQSVRQKQMLEQMLTDQMRSSVLSAQGQAHNTAAVTEKQOMLEQHLDQYKRVQDLEQMKVVE 226
 Qy 121 AMEYVQKLTLDELAWKRRHEIACGGPPRILCDBLLENMITSLSAESQLQTROQKLEE 180
 Db 227 AMEYVQKLTLDELAWKRRHEIACGGPPRILCDBLLENMITSLSAESQLQTROQKLEE 286
 Qy 181 LQOKVSYKGDPIVQHRPMLEFVLFNLMSAFAVVEROPCPMPMPDRPLVTKITGVQFT 240
 Db 287 LHQKQSYKGDPIVQHRPMLEFVLFNLMSAFAVVEROPCPMPMPDRPLVTKITGVQFT 346
 Qy 241 TVKRLILVKPELNTYQQLIKVCIKDQSGDVA 271
 Db 347 TVKRLILVKPELNTYQQLIKVCIKDQSGDVA 377

RESULT 3

A46159 interferon-dependent positive-acting transcription factor ISGF-3 91K chain - human
 C;Species: Homo sapiens (man)
 C;Accession: A46159
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 R;Schindler, C.; Fu, X.Y.; Imrta, T.; Aebersold, R.; Darnell Jr., J.E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 7836-7839, 1992
 A;Title: Proteins of transcription factor ISGF-3: one gene encodes the 91-and 84-kDa ISG
 A;Reference number: A46159; MUID:92365557; PMID:15020203
 A;Accession: A46159
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid; protein
 A;Residues: 1-739 <SCH>
 A;Cross-references: UNIPROT:P42224
 A;Experimental source: HeLa cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:110818)
 C;Superfamily: human signal transducer and transcription activator STAT5A
 C;Keywords: DNA binding protein APRF

Query Match 43.3%; Score 601.5; DB 2; Length 739;
 Best Local Similarity 45.8%; Pred. No. 3e-31; Matches 121; Conservative 55; Mismatches 73; Indels 15; Gaps 3;
 Qy 2 CLWERSRLQIATATAQGGQANHPTAAVTEKQOMLEQHLDQYKRVQDLEQMKVVE 61

RESULT 4

A56047 gamma-interferon activation site-binding protein Stat4 - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: A56047
 C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 R;Yamamoto, K.; Quelle, P.W.; Thiefelder, W.E.; Kreider, B.L.; Gilbert, D.J.; Jenkins, I
 Mol. Cell. Biol. 14, 4342-4349, 1994
 A;Title: Stat4, a novel gamma interferon activation site-binding protein expressed in ear
 A;Reference number: A56047; MUID:94277038; PMID:8007943
 A;Accession: A56047
 A;Status: preliminary; nucleic acid sequence not shown
 A;Cross-references: UNIPROT:P42228; GB:U09351; NID:9509502; PIDN:AAA19692.1; PID:9509503
 C;Superfamily: human signal transducer and transcription activator STAT5A
 C;Keywords: DNA binding; phosphoprotein

Query Match 42.0%; Score 582.5; DB 2; Length 748;
 Best Local Similarity 45.1%; Pred. No. 5.1e-30; Matches 120; Conservative 55; Mismatches 82; Indels 9; Gaps 3;

RESULT 5

A46160 interleferon alpha-induced transcription activator ISGF-3, 113K chain - human
 N;Alternate names: stat2 protein
 C;Species: Homo sapiens (man)
 C;Accession: A46160
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 R;Fu, X.Y.; Schindler, C.; Imrta, T.; Aebersold, R.; Darnell Jr., J.E.
 Proc. Natl. Acad. Sci. U.S.A. 89, 7840-7843, 1992
 A;Title: The protein of ISGF-3, the interferon alpha-induced transcriptional activator,
 A;Reference number: A46160; MUID:92365558; PMID:1502204

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA; protein

A;Residues: 1-851 <PUL>

A;Cross-references: UNIPROT:PS5630

A;Note: sequence extracted from NCBI backbone (NCBIP:110820)

R;Yan, R.; Ourshsi, S.; Zhong, Z.; Wen, Z.; Darnell, J.E.

submitted to the EMBL Data Library, December 1994

A;Accession: S71908

A;Molecule type: DNA

A;Residues: 1-851 <PAN>

A;Cross-references: EMBL:U18671; NID:g1293919; PIDN:AAA98760.1; PID:91293920

Nucleic Acids Res. 23, 459-463, 1995

A;Title: The genomic structure of the STAT genes: multiple exons in coincident sites in A;Reference number: S53873; MUID:95192056; PMID:7885841

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-196; 92-591; 684-730 <YAW>

A;Cross-references: EMBL:U18671

C;Genetics:

C;Gene: stat2

C;Superfamily: human signal transducer and transcription activator STAT5A

C;Keywords: signal transduction; transcription regulation

Query Match 26.2%; Score 364; DB 2; Length 851;

Best Local Similarity 33.7%; Pred. No. 6.5e-16; Mismatches 107; Indels 10; Gaps 6;

Matches 89; Conservative 58; MisMatches 107; Indels 10; Gaps 6;

QY 3 LWEESERILLOPATAAQOGGQANHPTAAVTEKQQ-MLEQHLDVQRKVQDQLRQMKVHEN 61

Db 112 LLEERKLILQKQRADEQE--PVLTPVSEQHEIESRLDRAMMEKLVKSISQKD 168

QY 62 LQDDDFPNYKULSKSGMDQINGANGNSVTQKMQQLEQMLTALQMRSTIVSELAGLISA 121

Db 169 QDPVCFRYK-IAQGKTPSLDPH--QTKEGKI - LQETNLBDKKEVKIDASLAGR 223

QY 122 MEYVOKTILTDELAKRREPIACGGPPNTCLDRLENWITSLAESOLQHOOQTKKLEEL 181

Db 224 LITTLEILL-PKLEWKAQOKACRAPIADGLEYQTWTFTAGAKLFLHQQLKELGL 282

QY 182 QQKVSYKGDPPIVQHRRPMLEERIVELFRNLMSAFVUTERQCPMPMPDRPVIVKTGVQFTT 241

Db 283 SCLVSYQDPLTKGYDLRNAQTELLQRLHRAFYVETQPCMPQTPHRPLIKTGSKFTV 342

QY 242 KVRLLVKKPELNYIQKIKVCKDK 265

Db 343 RTRLVLVRQEGNESTIYEVSIDRN 366

RESULT 6

I49274

mammmary gland factor - mouse

N;Alternate names: STAT protein homolog p80

C;Species: Mus musculus (house mouse)

C;Accession: 02-Jul-1995 #sequence revision 02-Jul-1995 #text_change 09-Jul-2004

R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Reference number: I49273; MUID:96004632; PMID:7568026

A;Accession: I49274

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-786 <RES>

A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JTA0; EMBL:248538; NID:9758633; PIDN:CA88420.1; PID:9758636

R;Mu, A.I.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin-3

A;Reference number: S54772; MUID:95237198; PMID:7720707

A;Reference number: S54772; MUID:95237198; PMID:7720707

RESULT 6

I49274

mammmary gland factor - mouse

N;Alternate names: stat5 protein

C;Species: Mus musculus (house mouse)

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S54772; I49273

R;Mu, A.I.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin-3

A;Reference number: S54772; MUID:95237198; PMID:7720707

A;Accession: S54772

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-793 <MTI>

A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JTA0; EMBL:248538; NID:9758633; PIDN:CA88420.1; PID:9758636

R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Reference number: I49273; MUID:96004632; PMID:7568026

A;Accession: I49273

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-793 <RES>

A;Cross-references: EMBL:U21103; NID:9747971; PIDN:AAA80590.1; PID:9747972

C;Genetics:

C;Gene: Stat5a

C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.5%; Score 2445; DB 2; Length 793;

Best Local Similarity 29.7%; Pred. No. 7.7e-11;

RESULT 7

S54772

mammmary gland factor - mouse

N;Alternate names: stat5 protein

C;Species: Mus musculus (house mouse)

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S54772; I49273

R;Mu, A.I.F.; Wakao, H.; O'Farrell, A.M.; Harada, N.; Miyajima, A.

EMBO J. 14, 1166-1175, 1995

A;Title: Interleukin-3, granulocyte-macrophage colony stimulating factor and interleukin-3

A;Reference number: S54772; MUID:95237198; PMID:7720707

A;Accession: S54772

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-793 <MTI>

A;Cross-references: UNIPROT:P42230; UNIPROT:Q9JTA0; EMBL:248538; NID:9758633; PIDN:CA88420.1; PID:9758636

R;Liu, X.; Robinson, G.W.; Gouilleux, F.; Groner, B.; Hennighausen, L.

Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Title: Cloning and expression of Stat5 and an additional homologue (Stat5b) involved in Proc. Natl. Acad. Sci. U.S.A. 92, 8831-8835, 1995

A;Reference number: I49273; MUID:96004632; PMID:7568026

A;Accession: I49273

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-793 <RES>

A;Cross-references: EMBL:U21103; NID:9747971; PIDN:AAA80590.1; PID:9747972

C;Genetics:

C;Gene: Stat5a

C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 20.5%; Score 2445; DB 2; Length 793;

Best Local Similarity 29.7%; Pred. No. 7.7e-11;

Matches 78; Conservative 46; Mismatches 110; Indels 29; Gaps 7;

Qy 1 RC---LWECSRILQATAAQCGQANHPTAAVTEKQMLQEQHQDVKRVDQLEQM 56
Db 107 RCIRHLINQFQLVREANNNGSSPAG---ILVADMSQKHQINQRPPEELRITQTEL 162

Qy 57 KVVENIQQDDPFNY-KTKSGDMQDLDLNMM-----QSVTROKMQQLRQML---TAL 104
Db 163 KKLQQTQEVFTIQYQBSLRIOQAQFQGLNQPERMSRETALQOKQVSLETWLOREAQTL 222

Qy 105 DQMRSSIVSELAGLISAMEVQVKLTDEELADWKERPEIACIGGPNICDRLENWITS 164
Db 223 QQRVTELAEKHQKTIOLRKQQTILDDELIQWKRQLAGNNGGPPEGSDLWQSCKL 282

Qy 165 AESQQTQRTQTKLKBELIQQKVSYKGDPIVQHRPMLEBERTVFLERNLMSAFVVERQCPM 224
Db 283 AEIIMONRQOIRRRAEHLCCQPIPG-PVEEMLAEVNATIDISALVTSPIERQ--- 338

RESULT 8

G02317 transcription activator stat5A - human
C;Species: Homo sapiens (man)
C;Accession: G02317
R;Lin, J.
A;Reference number: H01043
A;Accession: G02317
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-94 'LIN>
A;Cross-references: UNIPROT:P42229; EMBL:U43185; NID:gi151169; PID:AB06589.1; PID:g115
C;Superfamily: human signal transducer and transcription activator STAT5A

Query Match 18.2%; Score 252; DB 2; Length 794;
Best Local Similarity 28.5%; Pred. No. 9.5e-09; Mismatches 113; Indels 30; Gaps 8;
Matches 75; Conservative 45; Mismatches 113; Indels 30; Gaps 8;

Db 108 RCIRHLINQFQLVREANNNSAG---ILVADMSQKHQINQRPPEELRITQTEL 163

Qy 57 KVVENIQQDDPFNY-KTKSGDMQDLDLNMM-----QSVTROKMQQLRQML---TAL 104
Db 164 KKLQQTQEVFTIQYQBSLRIOQAQFQGLNQPERMSRETALQOKQVSLETWLOREAQTL 223

Qy 105 DQMRSSIVSELAGLISAMEVQVKLTDEELADWKERPEIACIGGPNICDRLENWITS 164
Db 224 QQRVTELAEKHQKTIOLRKQQTILDDELIQWKRQLAGNNGGPPEGSDLWQSCKL 282

Qy 165 AESQQTQRTQTKLKBELIQQKVSYKGDPIVQHRPMLEBERTVFLERNLMSAFVVERQCPM 224
Db 283 AEIIMONRQOIRRRAEHLCCQPIPG-PVEEMLAEVNATIDISALVTSPIERQ--- 338

Qy 225 MPHDPRLVIKGVQFTTKVRLV 247
Db 339 ----PQVLKTQTKFAATVRLV 356

RESULT 9

S55527 mammary gland factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55527; S43353
R;Wakao, H.; Gouilleux, F.; Groner, B.
EMBO J. 14, 854-855, 1995
A;Title: Corrigenda. Mammary gland factor (MGF) is a novel member of the cytokine regula

Query Match 9.3%; Score 129; DB 2; Length 837;
Best Local Similarity 25.6%; Pred. No. 0.81; Mismatches 90; Indels 80; Gaps 13;
Matches 70; Conservative 33; Mismatches 90; Indels 80; Gaps 13;

Qy 14 ATAAQCG-GQK-----NHPTAAVTT-----EKQQMLQEQ-HHQDVKRVQ 50
Db 66 ATAGEOGCKGNISLPLHTSTLESIYQDOPPLKVALTIQILQGKEKKAVIEFRILPGPFHKQ 125

Qy 51 D-----LEQRMKVENIQLDPEFYNTLKSQGMD----LGNMNSVTRQMKQ 95
Db 126 BELKETPLGLRHRYTRERLIRESLHGPCT--GQVSLQNLIDPPLNGPSPS----- 176

RESULT 11
 A54740
 interleukin-4-induced transcription factor stat - human
 C;Species: Homo sapiens (man)
 C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
 C;Accession: A54740
 R;Hou, J.; Schindler, U.; Henzel, W.J.; Ho, T.C.; Brasseur, M.; McKnight, S.L.
 Science 265, 1701-1705, 1994
 A;Title: An interleukin-4-induced transcription factor: IL-4 stat.
 A;Reference number: A54740; MUID:94367369; PMID:8085155
 A;Accession: A54740
 A;Status: Preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-848 <HOU>
 A;Cross-references: UNIPROT:P42226
 C;Superfamily: human signal transducer and transcription activator SRATSA
 C;Keywords: DNA binding; transcription regulation
 Query Match 9.3%; Score 129; DB 2; Length 848;
 Best Local Similarity 24.6%; Pred. No. 0.82; Matches 64; Conservative 40; Mismatches 104; Indels 52; Gaps 10;
 Matches 64;
 保守性 40; 错配数 104; 插入/删除数 52; 缺口数 10;
 64 5 EBSRLQQTAAQGGQANHPTAAWVTEKQQMLEQHQDQVRKVQDQEKKVNLQD 64
 73 EGSTILOHISTL--ESIYQRDPPLKIVAT----FROILOCKKKAV----MEQTHPLP 119
 65 DDFPNKYTKSQQGMDLNQNNQSV--TROMMQO-----LEQML-----TALDQMR 108
 180 AMLIQETTGEELEA---AKALVLRKIQIWERQQQLAGNGAP-----FEESLAPLQ 225
 120 PFIWQKEELKFKGIRRLQHRVGHLILRQLQKAEGQVSLHSIETPANGTGPSEAL 179
 109 RSTVSELAGLISAMYYVQKLTDERFLADRMRRPEACTIGSRPNICLDRLENWITLASEO 168
 169 LQTRQQIKKLELIOQKVSYKGDP-IQHRLMEEBIVELRNIMSAFVVERQCPMPHP 227
 228 DRPVVIKTSVQFTTRVRLV 247
 280 --POWLKIQTKFQACVRFLL 297

RESULT 12
 AB1947
 chromosome segregation protein [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Accession: AB1947
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AB1947
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, S.; Nakazaki, N.; Shimojo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AB1947
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:08YXT3; GB BA000019; PIDN:RAB73085.1; PID:gi17130474; GSPDB:G
 A;Residues: 1-1208 <KUR>

T27075 hypothetical protein Y51A2D.16 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Accession: T27075
 R;McMurray, A.
 A;Reference number: Z20307
 A;Accession: T27075
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residue: 1-1166 <WIL>
 A;Cross-references: EMBL:AL021497; PIDN:CAA16403.1; GSPDB:GN0023; CESP:Y51A2D.16
 A;Experimental source: clone Y51A2D
 C;Genetics:
 A;Gene: CESP:Y51A2D.16
 A;Map position: 5
 A;Intron: 17/3; 45/1; 76/2; 156/3; 240/2; 288/2; 594/2; 657/3; 756/3; 798/2; 900/3; 948
 Query Match 9 0%; Score 125 5; DB 2; Length 1166;
 Best Local Similarity 21.4%; Pred. No. 2;
 Matches 56; Conservative 51; Mismatches 80; Indels 75; Gaps 10;
 Qy 5 BESRLQIATAAQCGQANIFTAATVTEKQ---OMLEQHLD-----VR 46
 Db 413 DEAKKIQFELDEALE---ETSHVTRSSSERKHLKAKLE---LQDQEQAQTLLELNQKNG 468
 Qy 47 KRVQDLEQKMKVVENTQDDFPFPYKTKLSQODMQDINGNNOVSQTRQRMQOLEQMFTALDQ 106
 Db 469 KRLERBDQMTSNHNUKNEENDLKTCQTQLES-----KKLQRREDVLEKS 518
 Qy 107 MRRSTVSELAGILSAMEY---VOKLTDERLAD-----WKRPEPACTGGPP 150
 Db 519 RRADLIGRHSCTTSLINGANFEKINNDIDELIDNIDIMMNLAVAKRERDDRIQGQ 578
 Qy 151 NL-----CLDRLENMTSALSQSQLRQL---KLERBLOQKVSY 187
 Db 579 QIQELHDLDKRDIEKLRRSESESLLNESDDRVRELTRRNHMKEQVFLQEKRLNELST 638
 Qy 188 KGDPTIVQHREPMUBERIVELFRN 209
 Db 639 KNDDEI---DMVKASIEELRN 656

RESULT 15

H90279 microtubule binding protein, probable [imported] - *Sulfolobus solfataricus*
 C;Species: *Sulfolobus solfataricus*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: H90279
 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awavez, M.J.; Chantong, I.; Jeffries, A.C.; Kozena, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.; arratt, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
 submitted to GenBank April 2001
 A;Description: Sulfolobus solfataricus complete genome.
 A;Reference number: A99139
 A;Accession: H90279
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-464 <KUR>
 A;Cross-references: UNIPROT:Q9UXNA; GB:AE006641; NID:g13814451; PIDN:AAK41495.1; GSPDB:C
 C;Genetics:
 A;Gene: SS0126

Query Match 9 0%; Score 125; DB 2; Length 464;
 Best local Similarity 21.7%; Pred. No. 0.72; Mismatches 107; Indels 88; Gaps 15;
 Matches 73; Conservative 69; Mi matches 73; Gaps 15;

Qy 3 LWERSRLQIATAAQCGQANIFTAATVTEKQ---OMLEQHLD-----VR 468
 Db 92 LESTSKKLEQAVOELIEAQKHKDERITKLEESTTRKLEQAVQELIEAQKHKDERITKLEES 151

56 MKVVEN-LQDDDFENYK-----TUKSQGMDL---NNNQSVTR----- 91

Db 152 TKKLEQAVQELIEAQKHKDERITKLEESTTRKLEQAVQELIEAQKHKDERITKLE 211
 Qy 92 -QKMQQL-----EQMLTALDQMRSIVSBLAGLISAMLYVQKLT-----EGLADNK 138
 Db 212 EQAVQELIEAQKHKDERITKLEESTTRKLEQAVQELIEAQKHKDERITKLERSIOKLVAQ 271
 Qy 139 RRPEIACIGGPPNICLDRLENWITSLAESQIQTROOKIKUELOQKV-SYKG--DPIVQ 194
 Db 272 RRAEER-----IAKLENAVEQOLIVEQKRTDERITKLEEVTMKLVSQMGNEIRE 322
 Qy 195 HRPMI-----ERIVELFLRIMK-----SARVVEROPCPMPHEPDPLVX 234
 Db 323 LRKALGSMGRWGWRDFEKLIEIVBLAKOGLDLKVNKFY-----DDNGLFGL 374
 Qy 235 TGWOFTTKVRLVVKPELNTYQKICIDKSGYAA 271
 Db 375 KGVEY--DVDLIKOTKV-YLIEKSYVEKDUVWAA 408

Search completed: December 2, 2004, 23:53:10
 Job time: 42 secs